

UNIVERSIDAD COMPLUTENSE DE MADRID

FACULTAD DE CIENCIAS BIOLÓGICAS



**METABOLISMO DE LOS FENILPROPANOIDES Y
PROTEÍNAS RELACIONADAS CON LA PATOGÉNESIS
EN EL MECANISMO DE RESPUESTA DE UVA DE MESA
("VITIS VINIFERA" L. CV. CARDINAL) A ELEVADAS
CONCENTRACIONES DE CO₂ Y BAJAS
TEMPERATURAS**

**MEMORIA PARA OPTAR AL GRADO DE DOCTOR
PRESENTADA POR**


Irene Romero de la Fuente

Bajo la dirección de las doctoras
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A close-up photograph of a bunch of dark purple grapes hanging from a vine with green leaves. The grapes are in sharp focus, showing their individual shapes and colors. The background is slightly blurred, showing more of the vine and leaves.

**Metabolismo de los fenilpropanoides y
proteínas relacionadas con la patogénesis
en el mecanismo de respuesta de uva de mesa
(*Vitis vinifera* L. cv. Cardinal) a elevadas
concentraciones de CO₂ y bajas temperaturas**

**TESIS DOCTORAL
IRENE ROMERO DE LA FUENTE
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Memoria presentada por
IRENE ROMERO DE LA FUENTE
para optar al grado de
DOCTORA en CIENCIAS BIOLÓGICAS

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Para que conste a los efectos oportunos, firma el presente certificado en Madrid a 14 de diciembre de 2007.

M^a Teresa Sánchez Ballesta



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Carmen Merodio Moreno

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*“El futuro pertenece a los que creen
en la belleza de sus sueños”*

(Eleanor Roosevelt)

ABREVIATURAS

aa	Aminoácidos
ABA	Ácido abscísico
ACC	1-aminociclopropano-1-carboxilato
AFP	Antifreeze proteins
AOX	Alternativa Oxidasa
APX	Ascorbato peroxidasa
CA	Atmósfera controlada
CAT	Catalasa
CBD	Cysteine-rich chitin-Binding Domain
CBF	Cysteine Binding Factor
CHS	Chalcona sintasa
CoA	Coenzima A
COR	Cold –Regulated
HR	Humedad relativa
HSP	Heat Shock Proteins
HPLC-DAD-MS	Cromatografía de líquidos de alta eficacia-Detección Diodo Array-Espectrometría de Masas
JA	Ácido jasmónico
LEA	Late Embriogenesis Abundant
LOX	Lipooxygenasa
nsLTP	Proteínas transportadoras de lípidos no específicas
MAP	Empaquetamiento en atmósferas modificadas
MAPK	Mitogen-Activated Protein Kinase
MeJA	Metil Jasmonato
MeSA	Metil Salicilato
mRNA	RNA mensajero
PAL	L-fenilalanina amonio-liasa
Pb	Pares de bases
PEP	Fosfoenol piruvato
POD	Peroxidasa
PPO	Polifenol oxidasa
PR	Pathogenesis related
Put	Putrescina
ROS	Reactive oxygen species
SA	Ácido salicílico
SAR	Sistema de resistencia adquirida
SOD	Superóxido dismutasa
Spd	Espermidina
Spm	Espermina
STS	Estilbeno sintasa
UV	Ultravioleta

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Introducción

El empleo de tecnologías no contaminantes es necesario para dinamizar la oferta de productos hortofrutícolas frescos en las diferentes fases de producción, cosecha y postcosecha. En este sentido, es necesaria su incorporación en la fase de producción permitiendo una mayor biodiversidad, al mismo tiempo que se mantienen los rendimientos y se mejora el control fitosanitario reduciendo el uso de productos químicos. Una vez obtenidos productos frescos de calidad, los procesos de manejo postcosecha y la logística de la comercialización para mantener la calidad, garantizar la seguridad y reducir las pérdidas de producto, constituyen objetivos fundamentales en las actuales investigaciones en fisiología y tecnología postcosecha.

En el caso concreto de la uva de mesa, muy susceptible a las pérdidas de agua y a la infección fúngica causada principalmente por *Botrytis cinerea* Pers. durante su conservación a bajas temperaturas, las tecnologías postcosecha se centran en evitar la proliferación del hongo y en mantener los parámetros de calidad de la uva durante su periodo de vida útil.

1. CARACTERÍSTICAS Y PARÁMETROS DE CALIDAD DE UVA DE MESA

La uva o grano de uva es el nombre que recibe el fruto que crece formando racimos de la vid común. Pertenece al género *Vitis* de la familia Vitáceas, que incluye unas 600 especies de arbustos, por lo general trepadores y que producen frutos en baya. Dentro del género *Vitis* se incluyen unas 20 especies cultivadas por sus frutos y algunas por sus hojas que se consumen como verdura. Más del 95% de la producción total de uva proviene de la vid europea que pertenece a la especie *Vitis vinifera* L. y cuyas variedades se destinan principalmente a vinificación.

La composición de la uva varía según se trate de uvas blancas o tintas. En ambas destacan dos tipos de nutrientes: los azúcares (siendo la glucosa y la fructosa más del 99%

de los hidratos de carbono en el zumo de uva y constituyendo del 12 al 27% del peso fresco de la baya madura) (Hofacher et al., 1976), y las vitaminas (principalmente ácido fólico y vitamina B6). La fracción ácida de las uvas está formada principalmente por los ácidos tartárico y málico, constituyendo alrededor del 90% de la acidez total (Winkler et al., 1974). Otros ácidos orgánicos encontrados en proporciones variables pero siempre a bajas concentraciones son los ácidos cítrico (5-10% de la acidez total), succínico, fumárico, acético, glicólico, láctico, aconítico, quínico, siquímico y mandélico (Ruffner, 1982). Entre los minerales, el potasio es el más abundante y se encuentra en mayor cantidad en uva tinta; mientras que el magnesio y el calcio están en cantidades moderadas y son más abundantes en uva blanca. También abundan compuestos con reconocidas propiedades beneficiosas para la salud, tales como flavonoides, antocianos, y taninos, responsables al mismo tiempo del aroma, color, y textura característicos de estos frutos.

La uva de mesa es un fruto importante en la dieta mediterránea que se consume casi todo el año. El cultivo de uva de mesa en España supone un 2,6 % del total de uva cultivada. Según el Instituto Nacional de Estadística, la superficie agrícola destinada a la producción de uva de mesa en España en el año 2005 fue de 26445 Ha.

Las uvas, como otros frutos no climatéricos, no maduran después de cosechadas; alcanzando el óptimo de aceptabilidad en apariencia, sabor y textura mientras están en la vid. Su índice de madurez se ha basado, tradicionalmente, en el contenido de sólidos solubles (°Brix) y también en el valor de acidez titulable, así como en la relación azúcares/ácidos de las bayas (Guelfat-Reich y Safran, 1971). La apariencia es determinada principalmente por el color, especialmente en variedades coloreadas, en las que existen requerimientos mínimos que varían con la variedad y el grado estándar. El grado estándar designa el porcentaje de bayas por racimo, el cual debe mostrar una intensidad mínima de color y cobertura (Nelson, 1979). La cera de la superficie de las bayas es un factor de

calidad muy importante en la uva de mesa; la manipulación postcosecha en ocasiones destruye esta cera, haciendo que la piel esté más brillante que el efecto deseable que aporta la cera. El aroma es un carácter importante y complejo de la calidad de uva ya que es una mezcla de cientos de compuestos volátiles diferentes sintetizados durante la maduración (Gunata et al., 1985a,b; Strauss et al., 1986). Aunque los compuestos precursores de estas sustancias se encuentran en las hojas (Gunata et al., 1986), la síntesis y evolución del aroma tiene lugar en las bayas; y de hecho, las sustancias aromáticas están localizadas principalmente en la piel de las mismas (Winkler et al., 1974).

Las uvas están sujetas a serias pérdidas de vapor de agua, que causan desecamiento y oscurecimiento del raquis, roturas e incluso marchitamiento de las bayas y pérdida de peso del racimo (Nelson, 1979). Por esto, los racimos deben ser enfriados lo antes posible después de la cosecha. En este contexto, el “sudado” de la uva, como resultado de cambios drásticos y rápidos en la temperatura durante el almacenamiento, causa serios problemas asociados a la podredumbre por *Botrytis cinerea*, que es junto a las pérdidas de agua, uno de los principales responsables de las pérdidas postcosecha que determinan la vida útil de la uva de mesa (Lavee y Nir, 1986; Crisosto et al., 2002).

La uva de mesa cv. Cardinal se caracteriza por su color rojo violeta, presenta una pulpa jugosa y aromática y piel de espesor medio. Su maduración es temprana, variando desde mediados de julio a finales de agosto, dependiendo de las zonas. Aunque su origen es californiano, es una variedad muy cultivada en todo el mundo. En España, se cultiva en formas libres mayoritariamente en las provincias de Valencia, Alicante y Castellón, donde se obtienen unas producciones de aproximadamente 6000-7000 kg/Ha.

2. MECANISMOS IMPLICADOS EN LA INFECCIÓN Y RESPUESTA DEL FRUTO AL ATAQUE FÚNGICO

2.1. Factores intrínsecos implicados en el ataque fúngico

El hongo *Botrytis cinerea* es un patógeno necrotrófico que coloniza tejidos senescentes o muertos, pero debido a que es capaz de infectar también a bajas temperaturas, puede producir importantes pérdidas económicas durante la conservación en frío (Mansfield y Hutson, 1980).

Al igual que otros patógenos, *B. cinerea* utiliza 3 vías principales para penetrar en el tejido del huésped: (i) a través de aberturas naturales tales como lenticelas, finales de tallos e interfases pedicelo-fruto; (ii) por grietas directas de la cutícula del huésped que pueden ocurrir en cualquier momento durante el periodo de crecimiento y desarrollo del fruto; (iii) y a través de heridas causadas por agentes bióticos y/o abióticos durante el almacenamiento (Prusky y Lichter, 2007).

Los procesos de penetración pueden pasar desapercibidos para el huésped, o pueden promover rápidas señales de defensa que resultan en la inducción de compuestos de defensa para limitar el desarrollo del hongo. El periodo desde la infección hasta la activación del desarrollo del hongo y expresión de los síntomas se designa etapa quiescente (Prusky, 1996). Esta etapa podría ser el resultado de una respuesta localizada del huésped que se asocia a menudo con un “estallido oxidativo”, que da lugar a la producción de especies reactivas de oxígeno (ROS). La producción de ROS en las células ha sido también relacionada con los procesos de defensa de las plantas (Brisson et al., 1994). Se ha observado que tanto la inoculación del pericarpo de aguacate con *Colletotrichum gloeosporioides* como el tratamiento de cultivos celulares de aguacate con el elicitor de la pared celular de *C. gloeosporioides*, aumentaron la producción de ROS (Beno-Moualem y

Prusky, 2000). También, se han descrito cambios en el pH tisular de los frutos asociados a los procesos de maduración e infección por patógenos (Wang et al., 2004). Los hongos son capaces de alcalinizar el ambiente debido a la secreción activa de amonio liberado en las reacciones de proteólisis y desaminación de los aminoácidos (Eshel et al., 2002). En el caso de *B. cinerea* la acidificación de los tejidos del huésped es debido a la secreción de ácidos orgánicos, concretamente de ácido oxálico (Rollins y Dickman, 2001; Manteau et al., 2003).

La transición de la etapa biotrófica a la necrotrófica-saprofítica parece estar relacionada con factores que son modulados a nivel intracelular y que están afectados por los nutrientes y el pH del ambiente. Cada uno de los compuestos secretados (ácidos orgánicos o amonio) juegan un papel fisiológico crucial en la iniciación del desarrollo necrotrófico. Existen varias especulaciones acerca de las vías por las cuales la secreción de ácidos orgánicos aumenta los centros de virulencia. El oxalato podría debilitar al huésped, al ser tóxico para él, lo que facilitaría su invasión. Asimismo, se ha propuesto como hipótesis que la quelación de calcio de la pared celular por parte del oxálico y ácidos glucónicos debilita la pared celular del huésped y facilita su penetración (Hadas et al., 2007). Finalmente, la secreción de oxalato podría suprimir la generación de ROS y las respuestas de defensa asociadas, contribuyendo de este modo a la activación del modo de desarrollo necrotrófico (Cessna et al., 2000).

2.2. Factores ambientales o extrínsecos implicados en el ataque por *Botrytis*.

Temperatura y humedad.

Estudios acerca de la viabilidad del hongo almacenado a bajas temperaturas demostraron que, mientras que la agresividad patogénica de los conidios de *B. cinerea* almacenados a -80°C era casi igual a la de los conidios frescos, ésta decrecía según

aumentaba la temperatura de almacenamiento (Gindro y Pezet, 2001). Puesto que la actividad de estos microorganismos continúa a bajas temperaturas, los frutos son susceptibles al progreso de la infección durante su conservación frigorífica.

La humedad relativa (HR) también afecta al desarrollo de la infección, pero su efecto es dependiente de la temperatura. Estudios con flores *Freesia* infectadas por *B. cinerea* a distintas condiciones de temperatura y HR mostraron que la infección fue severa en las plantas almacenadas a 5, 12 y 20°C a HR del 100%; mientras que no hubo lesiones cuando fueron almacenadas a HR de 80 a 90% a 5°C ni a 20°C (Darras et al., 2006). Por consiguiente, la temperatura de conservación y humedad relativa ambiental son parámetros esenciales a tener en cuenta a la hora de evitar la supervivencia y multiplicación de estos hongos.

2.3. Factores endógenos implicados en la respuesta a la infección. Respuestas fisiológicas, bioquímicas y moleculares inducidas en las plantas en respuesta al ataque fúngico.

Las plantas responden al ataque por patógenos mediante la inducción de diferentes mecanismos de defensa. Estos incluyen respuestas específicas que operan a través de la acción de moléculas señal tales como el ácido salicílico (SA), el ácido jasmónico (JA), o el etileno, y que generan la acumulación de proteínas relacionadas con la patogénesis (PRs, del inglés *Pathogenesis-Related proteins*), fitoalexinas, u otros compuestos fenólicos (Elad, 1997; Dong, 1998; Feys y Parker, 2000). Se ha observado un aumento en el contenido de la fitoalexina resveratrol en hojas y frutos infectados con el hongo (Jeandet et al., 1995). Asimismo, se ha observado la acumulación de barreras mecánicas como carbohidratos y glicoproteínas ricas en hidroxiprolina entre las paredes celulares para limitar la invasión de las hifas del hongo (Showalter et al., 1985).

El ácido abscísico (ABA) es una de las hormonas relacionadas con la interacción planta-patógeno. Se ha descrito que mutantes de tomate (*sitiens*) (*Lycopersicon esculentum* Mill. Cv Moneymarker) con niveles de ABA reducidos son mucho más resistentes al ataque por *B. cinerea* que las plantas de tipo salvaje (Audenaert et al., 2002). Por otro lado, estudios realizados en tomate con aplicaciones de ABA exógeno mostraron que aumentos en el contenido de ABA por encima del nivel basal no incrementaron la susceptibilidad de los frutos a *B. cinerea* (Achuo et al., 2006).

En *Arabidopsis*, se ha descrito que el pretratamiento con metil jasmonato (MeJA) causó una eficiente reducción de porcentaje de podredumbre causado por *Alternaria brassicicola*, *B. cinerea* o *Plectosphaerella cucumerina* (Thomma et al., 2000). Asimismo, mutantes de *Arabidopsis* (*npr1*), que presentaban alterada la resistencia frente a patógenos bacterianos y fúngicos, mostraron defectos en la acumulación, percepción o señal de transducción del SA. Los resultados mostraron que la resistencia local frente a *B. cinerea* requiere señales mediadas por etileno, jasmonato y SA (Ferrari et al., 2003).

A nivel molecular, se ha observado la acumulación de distintas proteínas PRs. Algunas de ellas son enzimas hidrolíticas capaces de degradar componentes de la pared celular de patógenos, como quitinasas o β -1,3-glucanasas. Los niveles de estas proteínas o su correspondientes actividades, incrementan en hojas de uva infectadas con *B. cinerea* (Derckel et al., 1999). También se han detectado incrementos en los niveles de distintos mRNAs que codifican PRs en hojas y/o granos como respuesta a los agentes causales de la podredumbre gris (Busam et al., 1997a) así como durante el proceso de desarrollo de la uva (Davies y Robinson, 2000). En fresa inoculada con *Colletotrichum*, se observó que la inducción de la expresión de genes de quitinasa de clase II estaba regulada diferencialmente en respuesta al patógeno (Anwar y Ding, 2004). La quitinasa CHV5, purificada de uva y que presenta gran homología con varias quitinasas de clase IV, parece

conferir una mayor protección frente a patógenos que la mayoría de las quitinasas estudiadas y fue capaz de inhibir hasta un 50% la germinación de los conidios de *B. cinerea* con una concentración de $7.5 \mu\text{g mL}^{-1}$ de proteína (Derckel et al., 1998). Por otro lado, en uvas Chardonnay infectadas con *Uncinula necator* se observó un aumento en los niveles de una proteína tipo taumatina (VvTL2) en comparación con las uvas no infectadas (Girbau et al., 2004).

Además de estas proteínas hidrolíticas, también se han observado aumentos en los niveles de expresión de los genes que codifican proteínas relacionadas con el metabolismo de los fenilpropanoides tales como la L-fenilalanina amonio-liasa (PAL) y la estilbeno sintasa (STS) (Sparvoli et al., 1994) como respuesta al ataque por patógenos en la vid. Bézier et al. (2002), además de analizar algunas PRs y la expresión de los genes que codifican las enzimas PAL y STS, clonaron y caracterizaron el gen que codifica la proteína inhibidora de la poligalacturonasa (PGIP), cuyos niveles de expresión se indujeron en respuesta a la infección por *B. cinerea*. PGIP inhibió la actividad de la poligalacturonasa secretada por los hongos fungitóxicos y aumentó la estabilidad de los oligagalacturónidos activos así como el elicitor *in vitro* (Cervone et al., 1989).

Se ha investigado el papel de los oligogalacturónidos (OGA), compuestos liberados de las pectinas de la pared en las células heridas, para inducir las respuestas de defensa en vides y su protección frente a *B. cinerea*. Estudios cinéticos con células de *Vitis* mostraron que los OGA inducen una rápida y transitoria generación de peróxido de hidrógeno (H_2O_2), seguida de un aumento en la expresión de genes que codifican proteínas implicadas en la ruta de los fenilpropanoides, y estimulan las actividades de quitinasa y β -1,3-glucanasa, lo que podría estar relacionado con una mayor respuesta de defensa de la planta frente al hongo (Aziz et al., 2004).

También se ha estudiado el papel del calcio en el mantenimiento de la estabilidad e integridad de la pared celular así como de la membrana plasmática en la piel de uva por medio de la quelación de sustancias pécticas (Chardonnet et al., 1997). Además, se ha observado que la aplicación exógena de calcio incrementa su contenido en bayas y aumenta la resistencia a *Botrytis* en racimos conservados a bajas temperaturas (Miceli et al., 1999). La mayor resistencia a *B. cinerea* se atribuyó a la participación de los iones de calcio en la estabilización de la estructura de la pared celular en hojas de *Vitis* (Bowen et al., 1992).

3. CONSERVACIÓN DE FRUTOS Y HORTALIZAS A BAJAS TEMPERATURAS

La conservación a bajas temperaturas, por encima de las de congelación, es una de las técnicas más utilizadas para mantener la calidad y prolongar el periodo de vida útil de frutos y hortalizas: reduciendo la tasa de respiración y disminuyendo tanto la pérdida de agua por transpiración como la producción de etileno y el desarrollo de microorganismos. Sin embargo, debido a la alta susceptibilidad de determinados productos hortofrutícolas de origen tropical y subtropical al daño por frío, o bien a consecuencia de la aplicación de temperaturas inferiores a la óptima de conservación (subóptimas) en frutos tolerantes a las bajas temperaturas, se pueden provocar importantes pérdidas de calidad del producto durante su conservación (Morris 1982; Jackman et al., 1989). La naturaleza y severidad de los síntomas de daño por frío depende de la especie, variedad, tejido y estado de desarrollo o maduración, así como de la intensidad y duración de la exposición a las condiciones de estrés (Salveit y Morris, 1990). En uva de mesa, el empleo de temperaturas próximas a 0°C, puede provocar en algunas variedades disfunciones fisiológicas que conducen a una pérdida de calidad. Uvas cv. Jingxiu almacenadas durante 3 días a -2°C, presentaron daños en la ultraestructura de las células del pericarpo, desórdenes en la lamela estromal de los

cloroplastos o plastidios, pérdida de paredes celulares y alteraciones en la membrana nuclear (Zhang et al., 2005). Además, en estas condiciones, el periodo de conservación de la uva de mesa es limitado debido a su gran susceptibilidad al ataque fúngico.

3.1. Respuestas fisiológicas, bioquímicas y moleculares asociadas a la conservación a bajas temperaturas.

A pesar de que existen distintas teorías en la bibliografía, la mayoría de los autores están de acuerdo en que el proceso de daño por frío debería considerarse en dos etapas: una primera etapa en que el daño ocurriría de forma inmediata por la exposición a una temperatura crítica, y posteriormente una segunda en la que se originarían otros procesos secundarios dependientes del tiempo y de la temperatura de exposición que conducirían a los síntomas visibles de la lesión (Raison y Lyons, 1986). Las diferencias en lípidos y ácidos grasos entre las distintas plantas determinarían sus diferentes susceptibilidades, de forma que el cambio de fase de un estado líquido-cristalino a un estado sólido-gel en los lípidos de membrana alteraría tanto la permeabilidad como la energía de activación de las enzimas unidas a membrana, explicando así las alteraciones metabólicas de estas células. La validez de la teoría sobre la fase de transición de los lípidos, ha sido cuestionada ya que se ha observado que, en las plantas susceptibles a los daños por frío, solamente entre el 2-5% de los lípidos sufren la fase de transición a temperaturas de daño por frío (Raison y Wright, 1983; Raison y Orr, 1986), por lo que no parece claro que un cambio en una pequeña fracción de lípidos pueda influir tanto en el desarrollo de los daños (Salveit y Morris, 1990). Otro aspecto problemático de esta teoría es que la temperatura a la cual tiene lugar la fase de transición en la membrana depende del grado de insaturación de los ácidos grasos de los lípidos. Además, no siempre existen diferencias en la composición de los lípidos de la membrana entre las especies sensibles y tolerantes (Patterson et al., 1978;

Priestley y Leopold, 1979). El mutante de *Arabidopsis thaliana* *fab1*, tolerante a las bajas temperaturas, contiene un elevado nivel de ácidos grasos saturados en fosfatidilglicerol, muy superior al que presentan especies sensibles al frío (Wu y Browse, 1995).

Aunque el “sensor” de las plantas a las bajas temperaturas no ha sido identificado definitivamente, los descubrimientos de los últimos años continúan apuntando, entre otros factores, hacia una disminución en la fluidez de la membrana (Beck et al., 2007). La cianobacteria *Synechocystis* PCC6803 tiene al menos dos sensores para bajas temperaturas, uno de los cuales es una histidina quinasa clásica, y posee los componentes proteicos Hik33 y Hik19 (Browse y Xin 2001). Debido a que no se han detectado homólogos a los genes *Hik33* y *Hik19* en plantas, se han propuesto conceptos alternativos a la percepción del frío. Uno de ellos sugiere que el aumento de la viscosidad de membrana afecta a los canales de Ca^{2+} , induciendo un aumento de la concentración de calcio citosólico, el cual sucesivamente activa una MAPK u otras cascadas de transducción de señales (Monroy y Dhindsa, 1995) (Fig. I).

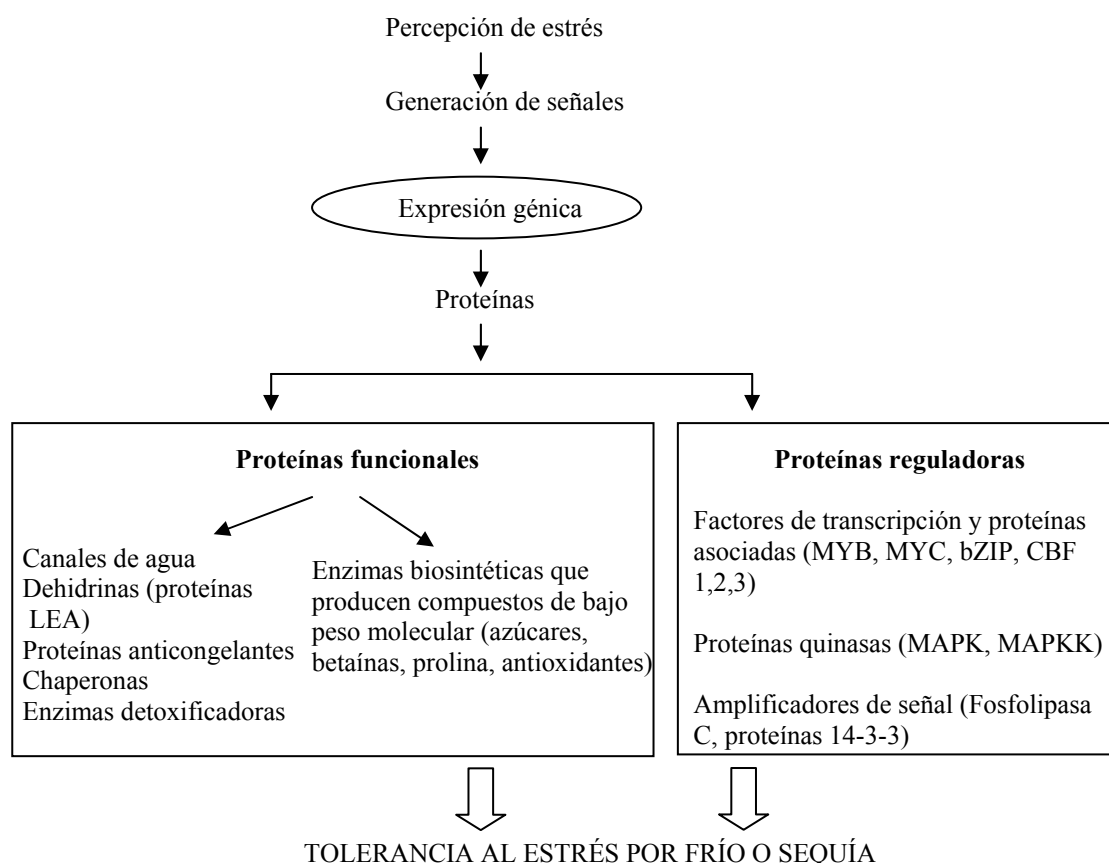


Fig. I. Factores de tolerancia a estrés producidos por las plantas en las respuestas adaptativas a bajas temperaturas y sequía.

A) Estrés oxidativo

Los estreses abióticos activan múltiples reacciones de defensa en las plantas, algunas de las cuales pueden proteger frente a distintos estreses. Las enzimas catalasa (CAT), superóxido dismutasa (SOD), ascorbato peroxidasa (APX), peroxidasa (POD) y glutathion reductasa (GR), pueden proteger frente al daño causado por radicales libres o ROS (como son el superóxido, el oxígeno singlete y el radical hidroxilo) generados por distintos estreses incluyendo las altas y bajas temperaturas (Wang, 1995). El almacenamiento a bajas temperaturas puede alterar el equilibrio entre la producción de radicales libres y los mecanismos de defensa a favor del primero. Así, el balance entre la formación y la detoxificación de ROS es crítico para la supervivencia de la célula durante

el almacenamiento en frío (Zhang et al., 1995). El complejo sistema antioxidante por el cual las plantas se protegen contra los efectos de las especies reactivas de oxígeno incluye, a parte de las enzimas mencionadas anteriormente, antioxidantes liposolubles (α -tocoferol y β -caroteno), reductores hidrosolubles (ascorbato y glutatión) (Zhang et al., 1995) y compuestos derivados de la ruta de los fenilpropanoides (fenoles, antocianos y estilbenos entre otros).

Las plantas que contienen niveles más elevados de antioxidantes, enzimáticos o no enzimáticos, son más tolerantes a las bajas temperaturas y otros tipos de estrés. La transformación de plantas de tabaco con el gen de la *Cu/Zn-SOD* de guisante indujo un aumento en la resistencia al estrés oxidativo causado por la exposición a las bajas temperaturas (3°C) en presencia de luz de intensidad moderada (Gupta et al., 1993). También se sabe que las plantas modulan sus defensas antioxidantes cuando se exponen a bajas temperaturas. Se ha observado un aumento en la actividad APX y POD en pimiento dulce (Yamauchi et al., 1975), y de SOD y CAT en tomate en respuesta al frío (Michalski y Kaniuga, 1981). En las variedades de manzana Golden Delicious y Fuji almacenadas en frío la actividad CAT se duplicó; mientras que la SOD disminuyó en Golden Delicious y aumentó en Fuji (Masia 1998).

En uva, los estudios realizados con enzimas antioxidantes están relacionados con la infección por distintos patógenos (Musetti et al., 2007). Hasta el momento no se ha estudiado la relación de estas enzimas con las bajas temperaturas.

B) Regulación proteica

Son numerosos los cambios fisiológicos y bioquímicos en frutos inducidos por la exposición a bajas temperaturas (Wang, 1990). Estos cambios podrían estar relacionados con modificaciones en la estructura terciaria de proteínas específicas (Linderstrom-Lang y

Schellman, 1959), con cambios en su actividad enzimática y en la población de mRNAs específicos (Watkins et al., 1990).

Con respecto al metabolismo de los fenilpropanoides, enzimas clave como la PAL y la chalcona sintasa (CHS) presentan cambios en su actividad (Sanchez-Ballesta et al., 2000; Wang et al., 2007) y en sus características cinéticas (Maldonado et al., 2007) como respuesta a las bajas temperaturas en diversos frutos. Como producto final de la ruta catalizada por la enzima PAL, se originan compuestos relacionados con la necrogénesis y con el pardeamiento de los productos vegetales (Dangyang y Salveit, 1989), así como otros compuestos implicados en la coloración, textura y capacidad antioxidante de los mismos. La inducción de la PAL se ha considerado un mecanismo de defensa frente distintos estreses bióticos y abióticos (Haga et al., 1988). En cítricos, se ha observado que el flavedo era capaz de responder al ataque por patógeno aumentando los niveles de transcrito de la *PAL* así como la actividad de la misma enzima (Ballester et al., 2006).

Las bajas temperaturas también pueden inducir cambios en enzimas hidrolíticas de la pared celular. El almacenamiento a bajas temperaturas (7°C) retrasó la maduración del aguacate (*Persea americana* Mill cv. Hass) y retardó la acumulación de mRNAs que codifican enzimas relacionadas con el metabolismo de la pared celular como celulasa, poligalacturonasa y enzima formadora de etileno (Dopico et al., 1993). Asimismo, se han descrito cambios en las actividades de las enzimas pectinolíticas en melocotones almacenados a bajas temperaturas, observándose un incremento en la actividad de la pectinesterasa así como una inhibición de la actividad poligalacturonasa (Ben-Arie y Sonego, 1980). La pectinesterasa es muy estable a bajas temperaturas y, en nectarinas conservadas en aire a 0°C, su actividad se mantuvo en un nivel basal de manera que el grado de esterificación de las pectinas continuamente disminuyó durante el almacenamiento (Lurie et al., 1994); mientras que la actividad de la poligalacturonasa fue

baja en estas condiciones. Estos cambios en las actividades de las enzimas hidrolíticas de pared podrían explicar parte de los cambios en la textura de los frutos durante su conservación a bajas temperaturas (Zhou et al., 2000).

C) Regulación Hormonal

C.1) Etileno

El incremento en etileno es una respuesta común de las plantas frente a distintos tipos de estrés, tales como las bajas temperaturas, sequía, heridas, irradiaciones, ozono y el ataque por patógenos (Yang y Hoffman, 1984). El hecho de que algunas de estas respuestas puedan ser inducidas por la aplicación exógena de etileno, sugiere que esta hormona pueda actuar como una señal que coordina las distintas respuestas de las plantas ante situaciones adversas (Wang et al., 1990). Se ha observado una estimulación considerable en la síntesis de etileno en frutos almacenados entre 0 y 5°C tales como melón (Lipton y Wang, 1987), tomate (Lurie y Klein, 1991), pera (Blankenship y Richardson, 1985) y mandarina (Zacarias et al., 2003).

En uva, Chervin et al. (2004) estudiaron la relación entre el etileno, el desarrollo y la maduración de los frutos, observando que, aunque la uva está clasificada como un fruto no climatérico, presenta un incremento transitorio de producción endógena de etileno justo antes de la averización. Por otro lado, Grimplet et al. (2007) analizaron la expresión de mRNAs que codifican proteínas implicadas en el metabolismo del etileno en piel de uva procedente de vides con déficit de agua y observaron una sobreexpresión significativa de los transcritos. Sin embargo, no existen, hasta el momento, datos en cuanto al papel de esta hormona en uvas almacenadas a bajas temperaturas.

C.2) Ácido abscísico y ácido giberélico

La exposición de los vegetales a bajas temperaturas puede afectar al estado hídrico de los mismos y, en consecuencia, a la producción de ABA (Walton, 1980), pero también puede afectar directamente a los niveles de esta hormona (Daie et al., 1981). El estrés por sequía incrementa la producción de ABA y produce el cierre de estomas e induce la expresión de genes asociados a estrés por sequía (Seki et al., 2007).

Se ha observado que entre las respuestas de las plantas para habituarse o aclimatarse al frío está el aumento del contenido de ABA y que este incremento es mayor en los tejidos que toleran mejor las bajas temperaturas (Ryu y Li, 1994). Asimismo, la aplicación exógena de ABA incrementa la tolerancia a las bajas temperaturas en distintas especies vegetales (Wang, 1990). El ABA endógeno producido por manzanas almacenadas a bajas temperaturas podría estar asociado con la tolerancia de las mismas al estrés por bajas temperaturas (Yoshikawa et al., 2007). Sin embargo, en mandarinas Fortune almacenadas en frío, se ha observado que los niveles de ABA pueden incluso disminuir tanto en las variedades tolerantes como en las variedades sensibles al frío (Lafuente et al., 1997; Lafuente y Sala, 2002).

Además de los reguladores mencionados anteriormente, el aumento en la tolerancia a las bajas temperaturas se ha asociado con variaciones en ácido giberélico. En uva de mesa almacenada en frío y tratada con 100 ppm de ácido giberélico, se ha observado que los frutos mantuvieron una mayor integridad de la membrana y que se redujo notablemente la caída de fruto, el pardeamiento del raquis y la podredumbre. Además, se observó una disminución en el contenido de sólidos solubles y vitamina C, así como una mejoría en la firmeza de la uva respecto a los frutos control (Deng et al., 2006).

D) Mecanismos moleculares

Se han identificado un gran número de genes regulados por las bajas temperaturas, algunos con una posible función reguladora y otros de función desconocida hasta el momento (Lee et al., 2005). Sin embargo, debido a que la mayoría de los estudios realizados se han hecho a nivel de planta, se sabe poco de los cambios moleculares que ocurren en los frutos durante su almacenamiento a bajas temperaturas.

Estudios comparativos han podido relacionar el aumento en los niveles de expresión de mRNAs homólogos a genes inducidos por las bajas temperaturas con las diferencias en tolerancia al frío de algunos cultivares. Estos incluyen genes *COR* (del inglés *cold-regulated*), que codifican un conjunto de pequeñas proteínas hidrofílicas denominadas dehidrinas o LEAs (del inglés *late embryogenesis abundant*) (Close, 1997); genes implicados en la biosíntesis de proteínas con función crioprotectora y/o anticongelante (AFPs, del inglés *Antifreeze Proteins*) (Hon et al., 1994) y genes relacionados con la defensa de las plantas frente al estrés oxidativo (Sung et al., 2003). Además se ha identificado y caracterizado un activador transcripcional de elementos promotores de varios genes *COR* (*CBF1*) (Jaglo-Ottosen et al., 1998) y genes implicados en la desaturación de ácidos grasos, relacionados con la adquisición de la tolerancia al frío en plantas de tabaco (Kodama et al., 1995).

Las LEA fueron las primeras proteínas relacionadas con la respuesta a la deshidratación en plantas (Baker et al., 1988). Desde entonces, se ha descrito en numerosos tejidos vegetales la posible relación entre la acumulación de este tipo de proteínas y la aclimatación de las plantas al estrés por frío (Bray 1993). La expresión de genes que codifican proteínas del tipo *dehidrina* (grupo 2 de las LEA), a menudo se induce en los tejidos vegetales como respuesta a la deshidratación, al estrés por bajas temperaturas o a la aplicación de ABA. Por ello se ha sugerido que podrían interactuar y estabilizar

membranas y macromoléculas, previniendo daños estructurales y manteniendo la actividad de enzimas esenciales (Svensson et al., 2002). Aunque las dehidrinas están ampliamente distribuidas y se han encontrado en plantas vasculares, helechos, musgos, líquenes y algas, sus funciones moleculares no son bien comprendidas ya que no catalizan ninguna reacción metabólica (Beck et al., 2007). Dehidrinas de cítricos (Hara et al., 2001; Sanchez-Ballesta et al., 2004), melocotón (Winiewski et al., 1999), trigo (Houde et al., 1995), cebada (Bravo et al., 2003) y espinaca (Kazuoka y Oeda, 1994) presentan actividad crioprotectora, así como actividad anticongelante en el caso de la dehidrina de melocotón (Winiewski et al., 1999). En hojas de *Vitis riparia* y *Vitis vinifera*, la deshidratación, las bajas temperaturas y el tratamiento con ABA indujeron la expresión de dos dehidrinas (Xiao y Nassuth, 2006).

Estudios realizados *in vitro* con cereales tolerantes a las bajas temperaturas como centeno, trigo y cebada han demostrado una acumulación de proteínas AFPs (Antikainen y Griffith, 1997). Este tipo de proteínas presentan un porcentaje de homología muy alto con PRs, en concreto con endoquitinasas de clase I, β -1,3-glucanasas y taumatina (Hon et al., 1994).

En *Arabidopsis*, se ha observado que los factores de transcripción CBF/DREB1 son reguladores críticos de la expresión génica en la señal de transducción de aclimatación al frío. Estos factores de transcripción han sido los primeros activadores transcripcionales en los que se ha demostrado su papel controlando la expresión de genes regulados por las bajas temperaturas (Thomashow, 1999; Van Buskirk y Thomashow, 2006). Sin embargo, Haake et al., (2002) aislaron un homólogo de las proteínas CBF/DREB1 (CBF4), que juega un papel similar durante la adaptación a la sequía, pero su expresión génica no está regulada por las bajas temperaturas. En uva (*Vitis vinifera* y *Vitis riparia*) la expresión de tres genes que cofican CBFs fue baja a temperatura ambiente y aumentó durante el tratamiento con bajas temperaturas (4°C) en hojas jóvenes, cabezas apicales, yemas y tallos

jóvenes. Los transcritos de *VvCBF1*, 2 y 3 que también se acumularon en respuesta a sequía y tratamientos con ABA exógeno, podrían indicar que la uva contiene genes *CBF* únicos (Xiao et al., 2006).

Otros genes cuya expresión se induce por las bajas temperaturas codifican polipéptidos que presentan homología con proteínas transportadoras de lípidos (nsLTP) (del inglés *non-specific lipid transfer*). Experimentos con gramíneas demostraron una acumulación de estas proteínas cuando las plantas fueron expuestas a condiciones de estrés hídrico, salino o por frío (Hughes et al., 1992; White et al., 1994).

También se ha identificado una espermidina sintasa (*OsSPDS2*) implicada en la síntesis de poliaminas en raíces de plantas de arroz asociada a la respuesta a las bajas temperaturas (Kim et al., 2004). Dicha implicación se ha confirmado en plantas transgénicas de *A. thaliana* que sobreexpresaban un gen de *SPDS* y que resultaron ser más tolerantes al frío (Kasukabe et al., 2004).

E) Otros compuestos endógenos

E.1) Poliaminas

Las poliaminas son pequeñas moléculas que pueden participar en distintos procesos como la regulación de la replicación del DNA, transcripción de genes, división celular, el desarrollo de órganos, maduración, senescencia y en respuesta a diferentes estreses bióticos y abióticos (Bouchereau et al., 1999). Putrescina (Put), espermidina (Spd) y espermina (Spm) son las poliaminas más abundantes en bacterias, plantas y animales. La hipótesis de que la síntesis de poliaminas puede estar relacionada con la defensa de los tejidos vegetales al frío, está basada en la capacidad de estos compuestos para estabilizar las membranas celulares (Wang, 1987). Asimismo, se piensa que su modo de acción frente

al estrés y la senescencia puede ser debido a la capacidad para secuestrar radicales libres que se forman en la peroxidación de lípidos (Drolet et al., 1986).

Los niveles de las poliaminas en los tejidos vegetales varían en respuesta al estrés hídrico (Wang y Steffens, 1985), osmótico (Tiburcio et al., 1990) y a las bajas temperaturas (Wang, 1987; Escribano y Merodio, 2000). En general, durante la exposición de frutos a bajas temperaturas, disminuyen los niveles de Spd y Spm y aumentan los niveles de Put (Serrano et al., 1996), al igual que en otros tipos de estrés (Bouchereau et al., 1999). La síntesis de ciertas poliaminas endógenas se puede ver incrementada por la aplicación exógena de las mismas, así como por el empleo de algunos tratamientos de acondicionamiento, lo que aumenta la tolerancia de los productos vegetales al frío. Así, en melocotones tratados con Put y almacenados a 2°C, se vio que aumentaba la firmeza de los frutos y se redujo la susceptibilidad del fruto a ser dañado mecánicamente (Martínez-Romero et al., 2000). En uvas, los estudios se han centrado en el análisis de las distintas poliaminas (libres, conjugadas y ligadas a pared) en órganos de la variedad Cabernet Sauvignon en diferentes estados del desarrollo. Se han observado diferencias en la distribución de las poliaminas en función de los órganos estudiados, y del estado de desarrollo en que se encontraban; pero, en general, se han encontrado niveles bajos de poliaminas en todos los órganos de la fruta en etapa de maduración (Geny et al., 1997). También se han estudiado las poliaminas como respuesta al ataque por hongo en distintos órganos (yemas florales, flores y bayas pequeñas) de vides Cabernet Sauvignon; y se ha descrito un aumento de las poliaminas ligadas a pared y una disminución de las libres en los órganos dañados (particularmente Put y diaminopropano) (Rifai et al., 2004). Hasta el momento se desconoce el papel de las poliaminas en el mecanismo de respuesta de las uvas a las bajas temperaturas.

E.2) Betaína glicina

La betaína glicina es una amina anfotérica cuaternaria que parece proteger las plantas manteniendo el balance de agua entre las células y el ambiente, y mediante la estabilización de la estructura y actividad de las macromoléculas (Sakamoto y Murata, 2002). Algunas plantas como la espinaca y la cebada, acumulan un nivel relativamente alto de betaína glicina en sus cloroplastos, mientras que otras, tales como *Arabidopsis* y tabaco, no sintetizan este compuesto (Sakamoto y Murata, 2002). Plantas de *Arabidopsis* transgénicas que expresaron genes de glicina sarcosina metiltransferasa (*ApGSMT*) y dimetilglicina metiltransferasa (*ApDMT*) procedentes de cianobacterias halotolerantes, acumularon altos niveles de betaína glicina e incrementaron su tolerancia a estreses de sequía, alta salinidad y bajas temperaturas (Waditee et al., 2005).

E.3) Ácido salicílico y ácido jasmónico

Recientemente, también se ha centrado la atención en el SA debido a su habilidad para inducir termotolerancia en plantas de mostaza (Dat et al., 1998, a,b), o proteger contra el estrés por bajas temperaturas en plantas de maíz (Janda et al., 1999), tomate (Ding et al., 2002) y trigo (Tasgin et al., 2003). El SA podría estar relacionado con el estrés oxidativo jugando un papel esencial en prever el daño oxidativo (Bowler et al., 1994). Uno de los modos de acción propuestos para el SA es la inhibición de la CAT, una de las enzimas eliminadoras de H₂O₂, de manera que las concentraciones celulares de H₂O₂ aumentarían y actuarían como mensajero secundario activando genes asociados a defensa (Chen et al., 1993). Shulaev et al. (1997) demostraron que el metil salicilato (MeSA) podría actuar como una señal aérea, la cual activaría la resistencia al daño y la expresión de genes asociados a defensa en plantas vecinas y en tejidos sanos de plantas infectadas. En manzanas almacenadas a bajas temperaturas (-2°C), se observaron mayores

concentraciones endógenas de JA que en las manzanas control mantenidas a 20°C (Yoshikawa et al., 2007). Esto sugiere que el JA podría estar asociado con la tolerancia de las manzanas al estrés por bajas temperaturas.

E.4) Azúcares y polialcoholes

La desecación que puede ocasionar el almacenamiento a bajas temperaturas se ha correlacionado con la acumulación de ciertos azúcares (tipo galactinol, trehalosa y fructano) y polialcoholes (como manitol y D-ononitol) (Bartels y Sunkar, 2005). Plantas de *Arabidopsis* transgénicas que sobreexpresaron *CBF3/DREB1A* fueron tolerantes a estreses de sequía y frío (Avonce et al., 2004), y acumularon más galactinol y rafinosa que las plantas de tipo salvaje (Valliyodan y Nguyen, 2006).

4. TECNOLOGÍAS PARA LA CONSERVACIÓN DE UVA DE MESA. TRATAMIENTOS GASEOSOS.

Para evitar el uso de fungicidas sintéticos y cubrir la demanda del consumidor, surge la necesidad de disponer de tratamientos alternativos no químicos que preserven la calidad postcosecha de frutos.

4.1. Generadores de dióxido de azufre

El dióxido de azufre (SO₂) se emplea en frutos mínimamente procesados para evitar procesos fermentativos, la aparición de mohos y pardeamientos (Jiang et al., 2002). El tratamiento con SO₂ y bajas temperaturas utilizado para la conservación de litchis (*Litchi chinensis* Sonn), aumentó el periodo de vida útil y disminuyó el pardeamiento de los mismos (Ray et al., 2005).

La fumigación con SO₂ es el método más comúnmente utilizado para controlar podredumbres durante la conservación en frío de racimos de uva (Harvey y Uota, 1978; Crisosto et al., 1994). Al principio, el SO₂ se aplicó a uva de mesa en altas concentraciones en exposiciones cortas de tiempo o en bajas concentraciones y exposiciones prolongadas. A mediados de los años sesenta, la exposición continua de uvas a SO₂ por largos periodos de tiempo se consiguió gracias al desarrollo de generadores químicos de fase doble (rápido y lento) (Nelson y Ahmedullah, 1972, 1976). Estos generadores pueden producir SO₂ durante varias semanas en ambientes refrigerados y con alta humedad (Lagunas-Solar et al., 1992). El almacenamiento de cultivares de uva de mesa a 2°C con generadores de SO₂ previno la podredumbre de la uva sin tener ningún efecto sobre la acidez, sólidos solubles o color, aunque su eficacia fue variable dependiendo del cultivar (Morris et al., 1992). Sin embargo, Crisosto et al. (2002) mostraron que la concentración de SO₂ necesaria para eliminar esporas y evitar el crecimiento del micelio inducía daños en la baya y el raquis. El nivel de SO₂ por encima del cual se han observado pérdidas en la calidad de uvas de mesa es de 10 mg/kg (Crisosto y Mitchell, 2002). Concentraciones elevadas de SO₂ producen blanqueamientos en la superficie de las bayas durante su almacenamiento y son especialmente visibles en variedades de uva de mesa tintas (Winkler et al., 1974). Además, los residuos de SO₂ son dañinos para la población alérgica a sulfitos, siendo 10 µL/L el umbral máximo tolerado para estos residuos presentes en frutos según la Administración de Drogas y Alimentos de los Estados Unidos (Crisosto et al., 1994); mientras que la Unión Europea ha prohibido su uso (EU Directive 95/2/CE). Por otro lado, no se puede emplear SO₂ en uvas certificadas de obtención orgánica (Gabler y Smilanick, 2001).

4.2. Atmósferas controladas

Las atmósferas controladas (CA, del inglés *Controlled Atmospheres*) contribuyen a mantener la calidad y prolongar el periodo de la conservación de productos vegetales (Beaudry, 1999). Niveles reducidos de O₂ y/o enriquecidos de CO₂ pueden reducir la respiración, retrasar la maduración, disminuir la producción de etileno, retardar el ablandamiento y ralentizar los cambios en la composición debido a la maduración, resultando todo esto en un aumento de la vida útil (Farber, 1991). Además de ser una tecnología postcosecha competitiva, el empleo de CA es una alternativa a la fumigación química (Yahia y Vazquez-Moreno, 1993). En los últimos años los progresos en su desarrollo tecnológico se han centrado en el empleo de fluidos criogénicos como el nitrógeno líquido que, además de favorecer el establecimiento de bajos niveles de O₂, actúan como medio de enfriamiento rápido (Mahajan y Goswami, 2007).

Los efectos de las CA con alto CO₂ en la calidad y fisiología de la uva han sido evaluados en distintas variedades (Artés-Hernández, et al., 2004; Crisosto et al., 2002). Estos resultados han mostrado que las CA pueden retardar la senescencia, reducir la respiración de la baya y del raquis, mantener la firmeza de la baya, disminuir el oscurecimiento del raquis y reducir, así como retrasar, la podredumbre. Sin embargo, las limitaciones del empleo del almacenamiento en CA son principalmente el metabolismo fermentativo y el estrés fisiológico que pueden dar como resultado el desarrollo de sabores y aromas anómalos, el oscurecimiento del raquis y la inducción de podredumbre por hongo después del paso a aire durante el periodo de vida útil (Grierson et al., 1966; Kader, 2002).

Métodos combinados de conservación tales como CA y generadores de SO₂ aumentaron el periodo de almacenamiento de los frutos, disminuyeron las pérdidas de peso, textura y color, y retrasaron tanto el ataque fúngico como el marchitamiento del

raquis (Pretel et al., 2006). Sin embargo, los niveles de ácido tartárico y cítrico mostraron un brusco incremento.

En uvas cv. Kyoho, el tratamiento con altas concentraciones de CO₂ y bajo O₂ suprimió las actividades de las enzimas celulasa, poligalacturonasa y peroxidasa; y como resultado se redujo la abscisión de las bayas de uva durante el almacenamiento (Deng et al., 2007). Las uvas cv. Thompson Seedles toleraron altos niveles de CO₂ durante más de 2 semanas a 0°C (Ahumada et al., 1996) y se consiguió un control adecuado de la infección por *Botrytis* usando altos niveles de CO₂ (Berry y Aked, 1997; Crisosto et al., 2002,b). En este mismo cultivar y en Red Globe se estudió la eficacia de atmósferas ricas en CO₂ sobre el control de podredumbre durante el almacenamiento de la uva a 0°C y se comparó con los generadores de SO₂. Se observó que concentraciones de 15% y superiores de CO₂ resultaron tan buenas como los generadores de SO₂ para controlar al hongo *Botrytis*; sin embargo, los tallos y pedicelos fueron más verdes cuando las uvas se almacenaron con generadores de SO₂ (Retamales et al., 2003).

4.3. Atmósferas modificadas

Las atmósferas modificadas (MAP, del inglés *packaging modified atmospheres*) pasivas o activas se presentan como una tecnología alternativa para la conservación de productos enteros o mínimamente procesados que presentan sensibilidad a distintos factores abióticos como las bajas temperaturas, altas o bajas HRs, etc. En estos casos, el almacenamiento en condiciones variables de composición gaseosa y humedad relativa de la atmósfera, permite aumentar el periodo de vida útil y mantener la calidad del producto vegetal. Generalmente, porcentajes de 3–8% CO₂ y 2–5% O₂ son recomendados para la conservación de frutas y verduras mediante MAP (Farber, 1991).

En cerezas, frutos no climatéricos altamente perecederos, se ha observado que la refrigeración de las mismas en MAP mejora ciertos parámetros de calidad del fruto (Apel et al., 1982), reduciendo las podredumbres causadas por desarrollo fúngico (De Vries-Patterson et al., 1991), inhibiendo el desarrollo del color de los frutos (Artés et al., 2001) y prolongando la vida postcosecha de los mismos (Remon et al., 2000).

El empleo de MAP se ha comprobado que mantiene la calidad organoléptica de uvas durante su almacenamiento. Sin embargo, la baja intensidad de respiración de la uva de mesa y por consiguiente las concentraciones de CO₂ alcanzadas dentro de los paquetes, no fueron lo suficientemente elevadas para actuar como fungicida (Martínez-Romero et al., 2003). Sin embargo, concentraciones de 15 kPa de O₂ y 10 kPa de CO₂ fueron eficaces para evitar el marchitamiento del raquis y el ablandamiento de los granos, así como para mantener la calidad visual, sabor y textura, controlando el desarrollo de podredumbres (Artés-Hernández et al., 2004).

Otros estudios mostraron que el empleo de MAP en combinación con ácido acético (Moyls et al., 1996), clorina (Zoffoli et al., 1999), eugenol (Valero et al., 2006) o generadores de SO₂ comercial (Artés-Hernández et al., 2004) en la conservación de uvas de mesa redujeron significativamente el daño provocado por *B. cinerea*; sin embargo, en estos estudios, el problema de los residuos persistió.

4.4. Ozono

La aplicación exógena de ozono permite el control del crecimiento y desarrollo microbiológico de los frutos así como de las instalaciones. Asimismo, retrasa la maduración de los frutos, lo que permite prolongar considerablemente el tiempo de conservación de los mismos. Además, la exposición a niveles de ozono por debajo de los críticos puede resultar en la inducción de compuestos de defensa, tales como estilbenos,

contra el estrés oxidativo (Roseman, 1991). Se ha observado que la aplicación de ozono, a lo largo de la conservación a bajas temperaturas de la uva de mesa, aumenta su contenido de fenoles totales (Artés-Hernández et al., 2007). Sin embargo, experimentos sobre fumigación con cantidades controladas de ozono revelaron que niveles bajos ($<0.15 \mu\text{L/L}$) afectan al crecimiento de las plantas y desarrollo, siendo los daños resultantes blanqueamientos, lesiones, clorosis y necrosis en las hojas de las plantas (Treshow, 1989). En tomate cherry, el tratamiento con altas concentraciones de ozono tuvo un efecto bactericida muy efectivo y no se observaron cambios en la textura; pero causó cambios en el color de la superficie de los mismos y podría resultar en pérdidas organolépticas y nutricionales (Das et al., 2006).

4.5. Jasmonatos y salicilatos

El JA y su ester metílico, MeJA, se han encontrado de forma natural en un amplio rango de plantas superiores. El JA es el producto final de la oxidación enzimática de ácidos grasos insaturados, linoleico y linolénico principalmente, y la enzima clave de esta ruta de los octadecanoides es la lipooxigenasa (LOX) (Vick y Zimmerman, 1984). Son fitohormonas lipídicas, que actúan como moléculas señalizadoras de la respuesta de las plantas a numerosas situaciones de estrés y participan en diversos procesos de desarrollo. La volatilidad del MeJA permite que los tratamientos sean aplicados sin necesidad de la inmersión del fruto en agua mientras que el JA, al ser más soluble en agua, es adecuado para usar en solución (Tripathi y Dubey, 2002).

Se ha demostrado que varios compuestos derivados del JA activan genes que codifican proteínas antifúngicas tales como tionina (Andresen et al., 1992), osmotina (Xu et al., 1994), y otros genes implicados en la biosíntesis de fitolalexinas (Gundlach et al., 1992). Se ha observado que el JA aumenta la tolerancia al estrés por frío de varias plantas

(Meir et al., 1996). En pimiento verde, se observó que el pretratamiento con vapores de MeSA o de MeJA indujo cambios en la expresión de genes que codifican la alternativa oxidasa (AOX) así como en las enzimas implicadas en la defensa frente al estrés oxidativo. El aumento de los niveles de los transcritos de AOX por MeJA o por MeSA se ha correlacionado con una menor incidencia de daño por frío (Fung et al., 2004).

Además, el tratamiento con vapores de MeJA redujo el porcentaje de infección causado por *B. cinerea* en fresa (Moline et al., 1997). También se observó que el tratamiento con bajas concentraciones de MeJA o de MeSA aumentaba substancialmente la resistencia de frutos de tomate al estrés por frío y disminuía la incidencia de podredumbre durante el almacenamiento a bajas temperaturas. Asimismo, dicho tratamiento indujo la síntesis de algunas proteínas asociadas a estrés, como PRs, que aumentaron la tolerancia al frío y la resistencia a los patógenos (Ding et al., 2002). En *Arabidopsis*, el pretratamiento con MeJA causó una eficiente reducción del desarrollo de infecciones fúngicas (Thomma et al., 2000).

Se ha descrito que el tratamiento exógeno con el análogo de JA, n-propil dihidrojasmonato, favorece el desarrollo del color de las bayas (Fujisawa et al., 1996). Además, recientemente se ha descrito que el tratamiento de hojas de *Vitis* con SA desencadenó el sistema de resistencia adquirida (SAR, del inglés *Systemic Acquired Resistance*) y fue efectivo para controlar la podredumbre (Aktas y Guven, 2007).

4.6. Otros tratamientos

a) Etanol y sorbatos

Etanol y sorbato potásico son conocidos aditivos de los alimentos con potente actividad antimicrobiana (Larson y Morton, 1991). Se ha descrito que los baños y vapores

en etanol son efectivos en la conservación postcosecha de melocotones, cítricos y uvas de mesa (Gabler y Smilanick, 2001; Karabulut et al., 2003). Los sorbatos son preservantes comunes de comida con muchas aplicaciones, y su espectro de actividad incluye *B. cinerea* (Sofos, 1989). Karabulut et al. (2005) analizaron el tratamiento combinado de etanol (20%) y sorbato potásico (0.5 ó 1%) en uvas de mesa cv. Flame Seedles para controlar el ataque por *B. cinerea* y observaron que la combinación de ambos compuestos tuvo igual eficacia en reducir la incidencia del hongo que los generadores comerciales de SO₂, pero sin observarse los daños en las bayas citados anteriormente para el tratamiento con SO₂.

b) Hexenal

El compuesto volátil (E)-2-Hexenal es ubicuo y fuertemente antifúngico, habiéndose demostrado su actividad contra *B. cinerea* (Fallik et al., 1998). Archbold et al. (1999) demostraron que es un fumigante eficiente en controlar el hongo de uvas de mesa apirenas. El vapor de hexenal inhibió el crecimiento de las hifas de *Penicillium expansum* y *B. cinerea* en ensayos *in vitro* y sobre rodajas de manzana (Song et al., 1996).

c) Ácido acético

La fumigación con ácido acético se ha demostrado que es adecuada para uso comercial de albaricoques y ciruelas (Liu et al., 2002), cerezas dulces (Chu et al., 2001) y uvas (Sholberg et al., 1996). El ácido acético es un intermediario del metabolismo fermentativo y se acumula en muchos frutos (Nursten, 1970). Sholberg y Gaunce (1995) mostraron que bajas concentraciones de ácido acético en aire fueron extremadamente efectivas para controlar los conidios de *B. cinerea* en manzanas sin tener efecto tóxico. Asimismo, la fumigación con ácido acético protegió del deterioro a las uvas conservadas en MAP a 0°C hasta 2 meses, y se presentó como una forma alternativa para aumentar su

tiempo de vida útil (Moyls et al., 1996). El empleo de ácido acético podría ser también una alternativa al SO₂, que se utiliza habitualmente para controlar la podredumbre de uvas de mesa.

d) Pretratamientos con CO₂

Pretratamientos con altos niveles de CO₂ sobre frutos tropicales y subtropicales durante la conservación a temperaturas inferiores a la crítica son efectivos en el control de los daños por frío (Merodio y De La Plaza 1997; Merodio et al., 1998). Cuando la aplicación de estos pretratamientos se realizó a temperatura ambiente se retrasaron los cambios asociados a la maduración y senescencia en los tejidos verdes (Merodio y De la Plaza, 1997; Escribano et al., 1997). También se observó una supresión de la síntesis basal y autocatalítica de etileno (sin modificar los bajos niveles de ACC oxidasa) y un incremento de los niveles de las poliaminas Spm y Spd (Muñoz et al., 1999).

En tomates cherry (*Lycopersicon esculentum* Mill.) conservados con altas concentraciones de CO₂ (20%) durante 3 días, y posteriormente transferidos a aire, se observó una inhibición de los cambios de color asociados a la maduración, una menor producción de etileno, así como una reducción del contenido de proteínas. También se observó una fuerte inducción de genes que codifican proteínas asociadas a estrés como una proteína de choque térmico (HSPs, del inglés *Heat Shock Proteins*) y una glutamato descarboxilasa (Rothan et al., 1997).

Por su carácter fungistático, el empleo de altas concentraciones de CO₂, se presenta como una alternativa al uso de SO₂ y de productos fitosanitarios. En este trabajo se estudia el efecto de un pretratamiento de 3 días de duración con altas concentraciones (20%) de CO₂ en la conservación de uva de mesa cv. Cardinal a bajas temperaturas. Se analizarán

distintos parámetros de calidad así como los mecanismos de respuesta de la uva asociados a la ruta de los fenilpropanoides y a las PRs durante estas condiciones de conservación.

Objetivos

El objetivo general de este trabajo es analizar las bases fisiológicas y moleculares implicadas en los mecanismos de respuesta de la uva de mesa cv. Cardinal al pretratamiento con 20% de CO₂ durante su conservación a 0°C.

Este objetivo general se ha desarrollado según los siguientes objetivos parciales:

1. Análisis de la efectividad del tratamiento con altos niveles de CO₂ para mantener la calidad de los diferentes tejidos del racimo de uva de mesa.

2. Análisis de los marcadores moleculares de la fase inicial de conservación a 0°C en la piel de uva de mesa y, de los principales mecanismos de protección inducidos por el tratamiento con altos niveles de CO₂ relacionados con el metabolismo de los fenilpropanoides.

3. Estudio de la eficacia del tratamiento combinado de bajas temperaturas y alto CO₂ en el control del ataque fúngico, y de la implicación de las proteínas relacionadas con la patogénesis. Estudio de la funcionalidad de una quitinasa y una β -1,3-glucanasa de clase I.

Capítulo 1

Efecto de elevadas concentraciones de CO₂ en los cambios metabólicos asociados con la respuesta de uva de mesa a 0°C. Metabolismo de fenilpropanoides.

Los compuestos fenólicos, productos secundarios del metabolismo de las plantas, contienen uno o más anillos aromáticos y, al menos, un sustituyente hidroxilo (Dixon, 2001). Constituyen un grupo heterogéneo de productos con más de 10000 compuestos, y esta diversidad estructural se debe a la gran variedad de modificaciones en regiones específicas, que incluyen hidroxilaciones, glicosilaciones, acilaciones, sulfataciones o metilaciones (Fridman y Pichersky, 2005). Por otro lado, se ha descrito que la concentración de los compuestos fenólicos en los frutos depende de factores genéticos, ambientales y culturales (Haselgrove et al., 2000).

El interés por estos compuestos se centra en su efecto beneficioso para la salud, debido en general a sus propiedades antioxidantes, lo que resulta en un efecto antiinflamatorio y un gran potencial en la prevención del cáncer y enfermedades cardiovasculares (Hertog et al., 1992). Diversos estudios epidemiológicos indican que el consumo de altas dosis de frutas y verduras aporta beneficios para la salud en la prevención de enfermedades crónicas (Arai et al., 2000). También se ha demostrado que los fenoles juegan un papel importante en la defensa de las plantas frente a distintos estreses bióticos y abióticos. Se ha descrito un aumento de antocianos y flavonas en respuesta a altos niveles de luz visible, y se piensa que éstos compuestos ayudan a atenuar la cantidad de luz que alcanzan las células fotosintéticas (Beggs et al., 1987). También la irradiación UV provoca un aumento de flavonoides (particularmente derivados de dihidrokaempferol) y esteroides de sinapato en *Arabidopsis*, así como de isoflavonoides en otras especies (Li et al., 1993; Lois, 1994). Algunos compuestos como las ligninas participan en la reparación de heridas y en el refuerzo de la pared celular, los flavonoides y/o las cumarinas protegen a las plantas del estrés oxidativo, y algunos compuestos fenólicos actúan como agentes antimicrobianos o antifúngicos (Dixon y Pavía, 1995; Ndong et al., 2003).

En los últimos años se ha prestado especial atención a los compuestos fenólicos por su implicación en la calidad de los productos hortofrutícolas (Bedgoog et al., 2005; Kalt, 2005) debido a la importancia que tienen en su aspecto y características organolépticas (Tomas-Barberán y Espin, 2001). Forman parte de esencias y pigmentos que confieren aromas, colores y sabores a los frutos; pero su degradación oxidativa catalizada por enzimas como polifenol oxidasa (PPO) y peroxidasa (POD) (Vamosvgyazo, 1981; Lei et al., 2004), es uno de los principales problemas de la industria alimentaria debido a que ocasionan el pardeamiento enzimático de frutos y vegetales frescos. La composición fenólica de los frutos y vegetales también puede ser afectada por las tecnologías de procesado de alimentos tales como tratamientos térmicos, presión, tratamientos enzimáticos, fermentación, etc. Además, procesados domésticos como cocinar (Price et al., 1998) y exprimir manualmente los frutos para obtener zumos (Häkkinen et al., 2000; Gil-Izquierdo et al., 2001) también afectan a su composición. Se ha descrito que la composición fenólica de la uva podría variar durante las diferentes etapas de desarrollo (Jordao et al., 2001), lo que podría ser atribuido a una serie de alteraciones químicas y enzimáticas de algunos fenoles durante la fase de maduración, que incluye la hidrólisis de glicósidos por glicosidasas, oxidación de fenoles por fenoloxidasas y polimerización de fenoles libres (Ryan et al., 2002).

1. Biosíntesis de los compuestos fenólicos

Aunque los compuestos fenólicos son un grupo heterogéneo desde el punto de vista metabólico, en su biosíntesis están involucradas dos vías básicas: la vía del ácido siquímico y/o la vía del ácido malónico (o de los poliacetatos).

La ruta del ácido siquímico, la principal en plantas superiores, es dependiente de luz y se inicia en los plastos por condensación de dos productos típicamente fotosintéticos,

la eritrosa 4-fosfato con el fosfoenolpiruvato (PEP), y por diversas modificaciones se obtiene el ácido siquímico, del cual derivan directamente algunos fenoles en los vegetales. La incorporación de una segunda molécula de PEP conduce a la formación de fenilalanina que, por acción de la enzima L-fenilalanina amonio-liasa (PAL), se transforma en el ácido *trans*-cinámico, sustrato común de la biosíntesis de distintos fenilpropanoides tales como antocianos, flavonoides, furanocumarinas antimicrobianas, fitoalexinas, ligninas y esteres fenólicos (Hahlbroock y Scheel, 1989; Dixon y Pavia, 1995). La ruta del ácido malónico, minoritaria en plantas superiores, da lugar a la síntesis de quinonas, xantonas y orcinoles, entre otros compuestos (Dixon y Pavía, 1995). Por otra parte, algunos de los compuestos citados anteriormente pueden originarse a través de rutas mixtas que combinan la ruta del siquimato y del malonato, como es el caso de los flavonoides (Dewick, 1994).

1.1. Enzimas reguladoras de la ruta de los fenilpropanoides: L-fenilalanina amonio-liasa, chalcona sintasa y estilbeno sintasa.

La enzima PAL cataliza la primera etapa en la ruta de los fenilpropanoides, que da lugar a una variedad de compuestos fenólicos con funciones relacionadas con estructura y defensa, que incluyen antocianos, pigmentos flavonoides, furanocumarinas, fitoalexinas, lignina y ésteres fenólicos (Hahlbroock y Scheel, 1989; Dixon y Pavía, 1995). Es la enzima clave del metabolismo de los fenilpropanoides y está regulada por distintos factores, tales como la luz, y depende además de la concentración de diferentes hormonas vegetales. En general, la actividad PAL aumenta cuando las plantas son sometidas a situaciones de estrés, como la falta de agua, infecciones fúngicas o bacterianas y radiaciones UV (Ohl et al., 1990). También se ha observado aumentos en la actividad de la PAL y acumulación de fenilpropanoides en plantas como respuesta a bajas temperaturas (Chalker-Scott et al., 1989; Leyva et al. 1995; Solecka et al. 1999; Janas et al., 2000; Sanchez-Ballesta et al.,

2000; Janas et al., 2002). Por otro lado, la manipulación de los frutos y vegetales durante la cosecha, el almacenamiento y el transporte postcosecha, pueden tener un importante impacto sobre los compuestos fenólicos y enzimas involucradas en el metabolismo fenólico, llevando a cambios (generalmente una disminución) en la calidad de los mismos (Tomás-Barberán y Espín, 2001).

En la mayoría de las especies estudiadas, la PAL está codificada por pequeñas familias multigénicas (Cramer et al., 1989) que se expresan diferencialmente en los tejidos de las plantas dependiendo de la respuesta a distintas condiciones de estrés (Lois et al., 1989). El gen que codifica la PAL así como otros genes de la biosíntesis de antocianos, han sido considerados como *cor*, y han sido propuestos como candidatos para caracterizar las respuestas moleculares de las plantas a las bajas temperaturas (Christie et al., 1994). Además de la regulación transcripcional, el estrés por frío puede también afectar a los niveles de los mensajeros de la PAL así como a su actividad enzimática (Graham y Patterson, 1982; Sanchez-Ballesta et al., 2000; LoPiero et al., 2005); aunque, en general, el nivel basal de transcritos de *PAL* y su actividad son bajos (Lee et al., 1994).

Estudios de la expresión de genes relacionados con la biosíntesis de antocianos en la piel de uva muestran que la ruta de formación de estos antocianos ocurre en dos fases. La mayoría de los genes que codifican las enzimas de la ruta (incluida la PAL) son expresados tempranamente en el desarrollo de la uva y ‘de novo’ después de la maduración, cuando se desarrolla el color. Además, no se ha detectado expresión de la *PAL* en la pulpa de uva en ninguna etapa del desarrollo (Boss et al., 1996).

La activación del metabolismo de fenilpropanoides podría jugar un papel importante en el desarrollo de barreras protectoras en las células dañadas por estrés. Así, plantas transgénicas con niveles de *PAL* suprimidos exhibieron necrosis espontánea (Tamagnone et al., 1998) o desarrollo más rápido y extenso de la lesión que las plantas

salvajes después de la infección por patógeno (Maher et al., 1994) sugiriendo que la inhibición de la biosíntesis de los fenilpropanoides podría comprometer el estado fitosanitario de la planta.

Un gran número de fenilpropanoides inducidos por estrés derivan del esqueleto flavonoide C15, el cual es sintetizado via chalcona sintasa (CHS) que cataliza la reacción de condensación de p-cumaril-coenzima A (CoA) y tres moléculas de malonil-CoA (Harbone y Grayer, 1988). La CHS es la enzima que cataliza el primer paso de la biosíntesis de los flavonoides. En la mayoría de las plantas, el producto inicial de la CHS es una tetrahydrochalcona que es posteriormente convertida a otras clases de flavonoides, tales como flavonas, flavanonas, flavanoles, antocianos (Holton y Cornis 1995) y 3-deoxiantocianidinas.

En estudios con uvas irradiadas con UV se ha observado que la expresión de mRNAs de CHS disminuyó en la piel de uva antes de la averización y aumentó después de la misma (Takayanagi et al., 2004). Aunque la actividad CHS es principalmente inducida por estímulos de luz (Schmelzer et al., 1988) y elicitores bióticos (Dixon y Pavía, 1995), se ha correlacionado con los mecanismos de defensa tras el estrés con ozono (Rosemann et al., 1991). Sin embargo, en líneas celulares procedentes de hojas de *Vitis* sometidas a tratamientos con ozono se observó actividad PAL mientras que no se encontraron evidencias de la implicación de la CHS en la respuesta a este gas (Sgarbi et al., 2003). Por otro lado, se han observado aumentos en los niveles de expresión de la PAL y CHS en respuesta a la infección por *Fusarium thapsinum* y *Curvularia lunata* en tejidos florales de sorgo (*Sorghum bicolor*) (Little y Magill, 2003). La acumulación coordinada de ambos mensajeros sugiere que las respuestas a los diversos estímulos bióticos y abióticos podrían ser reguladas a través de un mecanismo de control común (Loake et al., 1991).

La estilbeno sintasa (STS) es la enzima que controla la síntesis de fitoalexinas estilbénicas catalizando la última etapa de la biosíntesis de la ruta del resveratrol. La STS está codificada por una familia multigénica caracterizada por tener secuencias de nucleótidos con alta homología (Wiese et al., 1994); y es una enzima muy relacionada con la CHS ya que ambas enzimas son homodímeros que catalizan reacciones de condensación de p-cumaril-CoA con tres malonil-CoA pero con diferentes reacciones de ciclación.

Se ha descrito la expresión constitutiva de genes que codifican STS en uva (Sparvoli et al., 1994), pero esta enzima también puede ser inducida por factores abióticos como radiaciones UV, ozono o estreses bióticos (Dercks y Creasy, 1989; Adrian et al., 2000; Grimming et al., 2002). Así, la enzima STS es reconocida como el biomarcador más importante y susceptible inducido por ozono en vid y pino (Schubert et al., 1997). Además, la STS es una enzima de defensa frente al ataque fúngico. En *Vitis*, se han estudiado la STS y la PAL en respuesta a la infección por *B. cinerea* y se ha observado un incremento en la expresión de los genes tras la inoculación de las hojas con el hongo (Bézier et al., 2002).

1.2. Derivados fenilpropanoides: *trans*-resveratrol y antocianos

Los derivados fenilpropanoides son productos que tienen un papel específico en la respuesta frente a patógenos, como pantalla ultravioleta, mediante su capacidad antioxidante y de disipación de energía, así como componentes estructurales de la pared celular (Grace y Logan 2000). En uva los más destacados son los antocianos y el *trans*-resveratrol, pero también se deben mencionar las ligninas y suberinas responsables del engrosamiento de la pared celular como mecanismo de defensa.

La lignina y la suberina son polímeros complejos formados a partir de una mezcla de fenilpropanoides simples y su composición varía entre las distintas especies (Lewis y Yamamoto, 1990; Bernards y Lewis, 1992; Dixon y Pavía 1995). Estos compuestos

participan en el refuerzo de la pared celular haciendo así a las plantas más tolerantes frente a situaciones adversas; y también colaboran en los procesos de reparación de heridas contribuyendo, probablemente, a frenar el desarrollo de daños incipientes (Bernards y Lewis, 1992; Whetten y Sederoff, 1995).

Las fitoalexinas son un grupo de moléculas de estructura diversa, generalmente lipofílicas, no específicas en su actividad antifúngica y no muy potentes (Grayer y Harbone, 1994; Smith, 1996). El mecanismo de acción antimicrobiana de las fitoalexinas no se conoce bien todavía. La base de su toxicidad parece estar relacionada con la disrupción de membranas, aunque varios procesos fisiológicos y bioquímicos distintos a los cambios de permeabilidad de la membrana podrían también estar afectados (Rogers et al., 1996; Smith 1996). Las fitoalexinas no están presentes en tejidos de plantas sanas y son sintetizados a partir de precursores remotos en respuesta al ataque por patógenos o estrés, probablemente, como resultado de la síntesis de enzimas ‘de novo’ (Lamb et al., 1989).

En uva, la producción de fitoalexinas tales como estilbenos es una de las rutas de defensa más importantes (Langcake y Pryce, 1977). Las fitoalexinas de las especies de *Vitis* están formadas por un grupo restringido de moléculas que pertenecen a la familia del estilbeno y derivan principalmente del *trans*-resveratrol (3,5,4'-trihidroxiestilbeno). Este compuesto ha recibido últimamente mucha atención por su implicación en la salud humana (Bertelli et al., 1995; Jang et al., 1997; Hung et al., 2000); y se encuentra en las hojas de la vid y principalmente en la piel de las uvas. La producción de resveratrol depende de muchos factores y la concentración del mismo es muy dependiente del cultivar. Se acumula en respuesta a infección por hongo, radiación UV, o sustancias químicas (Langcake, 1981; Liswidowati et al., 1991; Jeandet et al., 1995; Adrian et al., 1997). Específicamente, ha sido estudiada la producción de *trans*-resveratrol en uvas y vino en respuesta a la irradiación con UV-C (Creasy y Coffee, 1988; Cantos et al., 2002). Además,

también se ha visto una buena correlación entre la producción de resveratrol y la resistencia al hongo gris (Sbaghi et al., 1995) y también al hongo negro causado por *Rhizopus stolonifer* en distintas variedades de uva (Sarig et al., 1997). El *trans*-resveratrol es sintetizado por la condensación de una molécula de p-cumaril-CoA con tres unidades de malonil-CoA en una reacción catalizada por la enzima STS. Estudios recientes muestran que el *trans*-resveratrol es fungitóxico a concentraciones fisiológicas contra *B. cinerea* (Adrian et al., 1998). Sin embargo, también se ha probado que aumenta la resistencia de las uvas a otros patógenos como *Plasmopara viticola* (Dai et al., 1995), *Phomopsis viticola* (Hoos y Blaich, 1990) o *Rhizopus stonifer* (Sarig et al., 1997). Este carácter antifúngico bastante inespecífico y la acumulación selectiva del *trans*-resveratrol en la piel de la uva, lo hacen un buen candidato como pesticida natural contra el ataque de patógenos ya que aumenta la resistencia natural de las uvas a la infección fúngica. Además, debido a sus propiedades antioxidantes, el *trans*-resveratrol puede también tener efectos positivos en la conservación de los frutos durante su almacenamiento. Como consecuencia de esto, tanto el aumento de la producción endógena como la aplicación exógena del mismo podrían ser explotados para reducir los daños de la uva (Montero et al., 2003).

Los antocianos son flavonoides glicosilados biosintetizados via siquimato (Mol et al., 1989), y como miembros del grupo flavonoide, comparten la estructura $C_6C_3C_6$. Son compuestos particulares entre los flavonoides debido a su habilidad para absorber luz visible, lo que resulta en su apariencia coloreada (Jackman y Smith, 1996). El término antociano (o antocianina) se refiere a las formas glicosiladas de manera natural de estos pigmentos; y sus agliconas son designados antocianidinas. La estructura esquelética de las antocianidinas es la 2-fenilbenzopirilo o catión flavilo, el cual es polihidroxlado y puede ser polimetoxilado (Jackman y Smith, 1996). Excepcionalmente, el catión flavilo lleva grupos hidroxilo en la posición 3, 5, 7, 4' (Brouillard, 1982). Hay 18 estructuras de

antocianidinas, de las cuales, las seis estructuras más comunes son: pelargonidina, cianidina, delphinidina, peonidina, petunidina y malvidina (Strack y Wray, 1994). Sin embargo, las antocianidinas están en pocas ocasiones en su forma libre en la naturaleza. En general, la glicosilación está siempre presente en la posición 3 del anillo C y confiere solubilidad y estabilidad a los antocianos (Brouillard, 1983). La fracción de azúcar ligado a las agliconas es principalmente glucosa, pero también pueden encontrarse otros monosacáridos como ramnosa, galactosa, xylosa, arabinosa o fructosa; disacáridos como rutinosa o soforosa y trisacáridos (Jackman y Smith, 1996).

La glicosilación imparte mayor solubilidad a las moléculas en agua (Mazza y Maniati, 1993) y tiene un fuerte impacto en el color. Los 3-glicósidos son, por ejemplo, más fuertemente coloreados que los 3,5- y 5-glicósidos, cuando se comparan sus densidades ópticas (Mazza y Maniati, 1993). Con respecto a esto, el color es más o menos independiente del tipo y número de azúcares en el C-3, mientras que una glicosilación adicional en el C-5 induce un ligero cambio hacia rojo-morado (Stintzing y Carle, 2004).

La distribución de los distintos antocianos es un rasgo característico de tejidos de frutos y otras plantas. Como otros compuestos fenólicos, se encuentran localizados en la vacuola celular (Harbone, 1967; Mazza y Miniati, 1993). Los antocianos son responsables del color rojo, violeta y azul de frutas y flores (Harbone y Grayer, 1988). Aunque se acumulan esencialmente en las células epidérmicas de flores y frutos, sus principales funciones parecen ser atraer insectos y pájaros para la polinización de las flores y de animales para la diseminación de las semillas de los frutos (Timberlake y Bridle, 1982). Además, los antocianos pueden ser factores importantes junto con otros flavonoides en la resistencia de las plantas frente al ataque de insectos (Harbone y Grayer, 1988). Por ejemplo, se ha descrito que la cianidina-3-glucósido era capaz de proteger hojas de algodón contra el gusano del tabaco (Hedin et al., 1983). Además, debido a su conocida capacidad

antioxidante, se han publicado distintos trabajos donde se describen ciertos beneficios terapéuticos asociados a los antocianos como propiedades antiinflamatorias y vasoprotectoras (Lietti et al., 1976; García-Alonso et al., 2004; Oak et al., 2006).

En uva, la biosíntesis de antocianos comienza con la maduración de la baya (averización) y normalmente continúa a través de la fase de crecimiento de la misma. Es un proceso controlado genéticamente, y se sabe que prácticas tales como el uso de fertilizantes, grado de carga del cultivo, grado de poda, así como la temperatura e intensidad de la luz (Kliewer 1970), afectan mucho a la expresión de enzimas de la ruta de flavonoides, induciendo la acumulación de antocianos (Dokoozlian et al., 1995). Además, se ha visto que las bajas temperaturas aumentan significativamente los niveles de antocianos en distintas especies de plantas (Faragher 1983; Christie et al., 1994; Oren-Shamir y Levi-Nissim 1997; Stiles et al., 2007). Otros factores como variedad, región y condiciones de crecimiento, también pueden influir en los niveles de antocianos producidos y en el perfil de los diferentes pigmentos (Mazza y Maniati, 1993).

2. Regulación de los fenilpropanoides

Se ha descrito la acumulación de mRNAs de *PAL*, *STS* y *CHS* en respuesta a estreses bióticos y abióticos (Leyva et al, 1995; Brehm et al., 1999; Sanchez-Ballesta et al., 2000; Versari et al., 2001). El almacenamiento a bajas temperaturas puede tener efectos positivos o negativos en los niveles de fenoles de los productos vegetales dependiendo del producto que se trate y de la temperatura de almacenamiento. En frutos rojos como fresas, arándanos, uvas y granadas, las bajas temperaturas producen un incremento del contenido de antocianos y de derivados del ácido hidroxicinámico que favorece el color del producto (Kalt y McDonald, 1996; Gil et al., 1997; Holcroft et al., 1998; Cantos et al, 2000). Sin embargo en productos sensibles al frío como la banana, la piña, el mango o el melón, el

almacenamiento a bajas temperaturas provoca la aparición de daños por frío, que coincide con un incremento en la actividad de la PPO y la POD (Ose et al., 1995; Stewart et al., 2001; Nguyen et al., 2003; Vela et al., 2003).

También los factores medioambientales y agronómicos afectan al contenido y composición de los compuestos fenólicos. En concreto, el estatus carbono-nitrógeno afecta al contenido de fenilpropanoides en plantas de tabaco (Fritz et al., 2006); y la deficiencia de boro también puede afectar sustancialmente al contenido fenólico de las plantas (Liakopoulos y Karabourniotis, 2005). Asimismo, la presencia de metales pesados (Tahlil et al., 1999), el estrés salino (Rodríguez-López et al., 2000), la deficiencia en calcio o fosfato (Juszczuk et al., 2004) y los pesticidas (Barth et al., 1995) pueden incrementar la actividad de enzimas del metabolismo de fenoles, y como consecuencia, aumentar la susceptibilidad al pardeamiento de los productos.

Como ya se ha mencionado anteriormente, el SA y el MeJA son moléculas implicadas en sistemas de transducción de señales, que inducen enzimas que a su vez catalizan reacciones biosintéticas para formar compuestos de defensa tales como compuestos fenólicos, entre otros (Ding et al., 2002). Así, el pretratamiento de células de perejil con SA aumentó la expresión de los genes que codifican la enzima PAL y la 4-cumarato:CoA ligasa (Thulke y Conrath, 1998). Pastírová et al. (2004) observaron que la aplicación de SA inducía la acumulación de cumarinas en plantas de manzanilla (*Matricaria chamomilla* L.). En uvas, Chen et al. (2006) demostraron que el SA podría activar la enzima PAL aumentando la acumulación de su mensajero, la síntesis de proteína “de novo”, la actividad enzimática y, en consecuencia, la acumulación de fenilpropanoides tales como ácidos fenólicos.

Estudios de la expresión de un gen *liPAL* aislado del tetraploide *Isatis indigotica* Fort., revelaron que las giberelinas, el ABA, el MeJA y los tratamientos con bajas

temperaturas, aumentaban los niveles de transcripción del mensajero (Lu et al., 2006). Además, se ha demostrado en zanahorias (Chalutz, 1973), cítricos (Riov et al., 1969, Lafuente et al., 2001) y manzanas (Faragher y Chalmers, 1977; Blankenship y Unrath, 1988), que el etileno es un regulador de la actividad PAL. La exposición de tejidos de plantas a niveles hormonales de etileno resultó en la inducción de la actividad PAL (Hyodo et al., 1991; Ritenour y Saltveit, 1996; Takahashi et al., 1996); y se ha observado que el daño mecánico puede también causar un aumento en la producción de etileno, con un correspondiente aumento en la actividad PAL (Ke y Saltveit, 1989). Asimismo, Martínez-Téllez y Lafuente (1997) sugirieron que el etileno podría estar implicado en el control de la actividad de la PAL en los frutos de mandarina Fortune almacenados a bajas temperaturas. Tratamientos realizados con 1-MCP, inhibidor de la acción del etileno, afectaron negativamente a la concentración de fenoles totales en la fruta madura. En este sentido, fresas tratadas con 1-MCP presentaron una disminución en la actividad PAL y la concomitante inhibición del incremento en la concentración de flavonoides y compuestos fenólicos (Jiang et al., 2001).

También ha sido muy estudiado el aumento de compuestos fenólicos como respuesta a la infección con distintos patógenos. Así, Arfaoui et al. (2007) comprobaron que el aumento en la acumulación de compuestos fenólicos, observado en la germinación de garbanzos inoculados con hongo del género *Fusarium*, podría ser atribuido a la mayor expresión de genes de la ruta de los fenilpropanoides, ocasionado por el pretratamiento con *Rhizobium*. En uva, se han detectado aumentos en el contenido de la fitoalexina resveratrol en hojas de vid y bayas infectadas por *B. cinerea* (Langcake y Mc Carthy, 1979; Jeandet et al., 1995). También se han visto aumentos en la expresión de los genes que codifican las enzimas PAL y STS en hojas de vid infectadas por *B. cinerea*, como mecanismo de

defensa de la planta frente al ataque por patógenos, pero la activación de estos genes no fue suficiente para detener la extensión del hongo (Bézier et al., 2002).

Por otro lado, los fenilpropanoides tienen un papel regulador sobre distintos procesos. Las moléculas mejor estudiadas en este sentido son los derivados glicosilados del dihidrokaempferol y de los flavonoides como potenciales reguladores de la división celular (Teutonico et al., 1991); los flavonoides como reguladores del transporte de auxinas (Jacobs y Rubery, 1988); y el SA como regulador de la expresión de genes que se inducen por infección de patógenos o por estrés oxidativo (Dempsey et al., 1999).

Dado que el metabolismo de fenilpropanoides es uno de los mecanismos de respuesta de las plantas frente a distintos estreses bióticos y abióticos, se estudió la implicación de enzimas claves de esta ruta (PAL, CHS y STS), así como sus productos derivados, antocianos y resveratrol, en la mejora de la calidad de la uva de mesa conservada a bajas temperaturas y altas concentraciones de CO₂.

ARTÍCULO 1

Effect of high CO₂ pretreatment on quality, fungal decay and molecular regulation of stilbene phytoalexin biosynthesis in stored table grapes

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RESUMEN

Uvas de mesa (*Vitis vinifera*) cv. Cardinal almacenadas a baja temperatura fueron analizadas para determinar el efecto del pretratamiento con 20 kPa O₂ +20 kPa CO₂ +60 kPa N₂ durante 3 días sobre la calidad y el ataque por hongo. El patrón de la expresión génica de la estilbeno sintasa (STS) y los niveles de *trans*-resveratrol fueron también analizados en uvas durante el almacenamiento a bajas temperaturas (0°C) y posteriormente durante el tiempo de vida útil a 20°C durante 2 días. Nuestros resultados mostraron que el pretratamiento con alto CO₂ fue efectivo para mejorar la apariencia de los racimos y mantener la calidad de los frutos. En los racimos tratados con CO₂, los índices de marchitamiento y oscurecimiento, la disminución en el contenido relativo de agua y la pérdida de peso fueron también menores que en uvas no tratadas. Los niveles de mRNA de *STS* y la acumulación de *trans*-resveratrol en uvas tratadas con CO₂ fueron mucho más bajos que en uvas no tratadas durante el almacenamiento a bajas temperaturas. Además, el patrón de expresión génica de *STS* y el contenido de *trans*-resveratrol en uvas de mesa tratadas con CO₂ fueron consistentes con la reducción del ataque por hongo, crecido de forma natural, producida por este pretratamiento. Este tratamiento efectivo no estresante evita la inducción del *trans*-resveratrol durante el almacenamiento a bajas temperaturas hasta que su síntesis es aumentada durante el tiempo de vida útil a 20°C.

Effect of high CO₂ pretreatment on quality, fungal decay and molecular regulation of stilbene phytoalexin biosynthesis in stored table grapes

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Abstract

Table grapes (*Vitis vinifera*) cv. Cardinal stored at low temperature were analysed to determine the effect of pretreatment with 20 kPa O₂ + 20 kPa CO₂ + 60 kPa N₂ for 3 days on quality and control of decay. The pattern of stilbene synthase (STS) gene expression and trans-resveratrol levels were also analyzed in grapes during low temperature storage at 0 °C and further shelf-life at 20 °C for 2 days. Our results showed that high CO₂ pretreatment was effective for improving appearance of the bunches and maintaining the quality of the berries. In CO₂-treated bunches the browning and withering index, the decline in relative water content and the weight loss were also lower than in non-treated ones. The levels of STS mRNA and the accumulation of trans-resveratrol in CO₂-treated grapes were much lower than in the non-treated grapes during low temperature storage. Moreover, the pattern of STS gene expression and trans-resveratrol content in CO₂-treated grapes was consistent with the reduction of natural total decay produced by this pretreatment. This effective non-stressing treatment avoids the induction of trans-resveratrol during low temperature storage until its synthesis is enhanced during shelf-life at 20 °C.

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Keywords: Table grapes; *Vitis vinifera*; Fruit quality; Postharvest technology; Carbon dioxide; Laser spectrometry; Stilbene synthase; Resveratrol

1. Introduction

Low temperature storage is one of the most effective technologies for extending the postharvest life of fruit and vegetables. However, in table grapes low temperature storage life is limited by high sensitivity to fungal attack, mainly from *Botrytis cinerea*. This pathogen, which has a considerable economic impact in horticulture, is usually controlled by means of fungicides, but this can lead to multiple resistance in the pathogen population (Raposo et al., 1996). Moreover, because postharvest chemical treatments are restricted in most countries, safe alternative control technologies need to be developed to assure high quality fruit and control fungal attack. Commercial alternatives to the use of SO₂ generators have been proposed to maintain the

quality of table grapes over the short term, using modified atmosphere packaging (MAP) alone or in combination with natural fungicides (Artés-Hernández et al., 2006). Also, the application of controlled atmospheres (CA) under a continuous flow has been reported to be beneficial for controlling postharvest diseases in table grapes for prolonged cold storage (Yahia et al., 1983). However, rachis browning places a limitation on prolonged storage under CA (Crisosto et al., 2002; Retamales et al., 2003). An alternative gaseous treatment would be pretreatment with high CO₂ concentrations for shorter storage periods during postharvest handling of table grapes. Considering the low risk of this treatment, the use of pretreatments with high CO₂ levels to control *Botrytis* storage rot in maintaining table grape quality could be an interesting area of research. However, we need to know the efficacy of pretreatment with high CO₂ levels in controlling decay and maintaining quality of both rachis and berries. We also need to know whether this treatment corre-

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lates with the activation of a number of defense mechanisms in grapes. In previous work, we reported that the expression of *Vitis* class I chitinase and β -1,3-glucanase genes is not enhanced with CO₂ treatments which control fungal decay, and we suggested that the efficacy of high CO₂ pretreatment on the reduction of fungal decay is not mediated by the induction of the above mentioned PR genes (Romero et al., 2006).

Among the other possible defense mechanisms, the induction of the phenylpropanoid pathway appears to play a crucial role (Hahlbrock and Scheel, 1989). In grapes, the production of phytoalexins such as stilbenes on the phenylalanine/polymalonate pathway (Langcake and Pryce, 1977) is one of the most important defense pathways. Phytoalexins from *Vitis* species are composed of a restricted group of molecules belonging to the stilbene family and deriving primarily from trans-resveratrol (3,4'-5-trihydroxystilbene). Trans-resveratrol, which has recently received a lot of attention because of its implication in human health (Bertelli et al., 1995; Jang et al., 1997; Hung et al., 2000), is mainly present in the skin of berries. Resveratrol production depends on many factors and the concentration is highly dependent on the cultivar. In grape tissues, trans-resveratrol production has been described after microbial infection or treatment with elicitors and several kinds of stress (Langcake and Pryce, 1976; Liswidowati et al., 1991; Jeandet et al., 1995). Specifically, production of trans-resveratrol in wine and table grapes in response to UV-C irradiation has been extensively studied (Creasy and Coffee, 1988; Langcake and Pryce, 1977; Cantos et al., 2002). Moreover, a good correlation has been reported between resveratrol production (as induced by UV-C elicitation) and grey mould resistance (Sbaghi et al., 1995), and also black mould caused by *Rhizopus stolonifer* on several table grape varieties (Sarig et al., 1997). Trans-resveratrol is synthesized by condensation of one molecule of 4-coumaroyl-CoA with three malonyl-CoA units in a reaction catalyzed by stilbene synthase (STS). This enzyme is encoded by a multigene family characterized by high nucleotide sequence homology (Melchior and Kindl, 1990; Wiese et al., 1994). A constitutive expression of STS has been reported (Sparvoli et al., 1994), but it could be expressed differentially in response to biotic and abiotic stresses (Preisig-Müller et al., 1999; Brehm et al., 1999; Versari et al., 2001).

The aim of this work was to analyze the effectiveness of pretreatment with 20% CO₂ in controlling natural postharvest decay and its effect on quality attributes of rachis and berries and the molecular regulation of stilbene phytoalexin biosynthesis. STS gene expression and trans-resveratrol content of table grapes cv. Cardinal during low temperature storage at 0 °C and further shelf-life at 20 °C for 2 days were monitored. These technological and molecular studies were based on the premise that an understanding of the role of high CO₂ levels in disease resistance and quality may contribute to the development of more effective postharvest technologies.

2. Materials and methods

2.1. Plant material

Table grapes (*Vitis vinifera* L. cv. Cardinal) were harvested at random in Camas (Sevilla, Spain) in July. Early-harvesting mature berries were used in this work (12.7% total soluble solids; 0.81% tartaric acid). After harvesting, field-packaged bunches were transported to the laboratory, where fruit were immediately forced-air precooled for 14 h at –1 °C. After cooling, bunches free from physical and pathological defects were randomly divided into two lots and stored at 0 ± 0.5 °C and 95% relative humidity (RH) in two sealed neoprene containers of 1 m³ capacity. Ten plastic boxes containing about 3 kg of table grapes per box were stored in each container. One lot was stored under normal atmosphere for 33 days (non-treated fruit) and the other under a gas mixture containing 20% CO₂ + 20% O₂ + 60% N₂ (CO₂-treated fruit) for 3 days. The CO₂ concentration was maintained throughout the pretreatment experiment and was measured daily using an automated gas chromatograph system equipped with a thermal conductivity detector and Poraplot Q column (Varian Chrompack CP20033P). After 3 days, CO₂-treated grapes were transferred to air under the same conditions as the non-treated fruit until the end of the storage period. At the end of low temperature storage (33 days), both CO₂-treated and non-treated grapes were transferred to ventilated storage containers for an additional 2 days at 20 °C and 95% RH, to simulate shelf-life during marketing. Ten clusters were sampled periodically during low temperature storage and at the end of their shelf-life. Berries obtained from five clusters (approximately 300 g each cluster) were peeled and the skin was frozen in liquid nitrogen, ground to a fine powder and stored at –80 °C until analysis. For quality parameters, 45 berries were used, randomly removed from five clusters and distributed in three replicates of 15 berries each.

2.2. Quality assessments and total decay

Bunch withering, browning indexes and the relative water status (RWC) of the stem were determined for each bunch. Bunch withering was determined using the following subjective scale: (0) none, (1) onset of withering in pedicel and apex of stem, (2) withering of pedicel, apex of stem and over 10% of the main stem, (3) withering in up to 50% of main stem, and (4) total withering of main stem. The scale used for the browning index was: (0) none, (1) slight, (2) moderate, (3) severe, and (4) extreme. The water status of the stem was followed by measuring the RWC. One centimeter of stem, cut with a razor blade was weighed fresh, again after 24 h rehydration with distilled water at room temperature, and finally after drying at 85 °C, to give the fresh (FW), turgid (TW) and dry (DW) weights, respectively. RWC was determined from the equation: $RWC (\%) = (FW - DW) / (TW - DW) \times 100$.

Berry quality assessment considered dry matter (DM), soluble solids content (SSC), pH, titratable acidity (TA) maturity

index (ratio SSC/TA), colour and total decay. The DM content (%) was determined in grapes cut longitudinally with a razor blade in four pieces, after drying at 65 °C to a stable weight after two subsequent weight measurements. SSC was determined using a digital refractometer Atago PR-101 (Atago Co. Ltd., Japan) at 20 °C and expressed in °Brix. The pH of the juice was measured in a pH meter with glass electrode. TA was determined by titration with 0.1N NaOH up to pH 8.1 and results were expressed in % tartaric acid.

The external colour of the berries was measured using the Hunter Lab System and a Minolta colorimeter CR200™ model (Minolta Camera Co., Osaka, Japan). The color space coordinates L^* , a^* , b^* and chroma (C^*) ($a^{*2} + b^{*2}$)^{1/2} were determined around the equatorial region in three different positions.

Total anthocyanins were extracted from frozen skin samples (0.5 g) four times with 0.5 mL methanol acidified with 0.01% (v/v) HCl under continuous ultra-sonication for 10 min and centrifuged at 2000 × *g* for 10 min each time. All steps were carried out at 4 °C. Anthocyanins contents were measured in the combined supernatant by the pH differential method (Wrolstad, 1976). The absorbance was measured with a Perkin-Elmer spectrophotometer (Norwalk, CT) at 510 and 700 nm in buffers at pH 1.0 and 4.5, using $A = (A_{510} - A_{700})_{\text{pH } 1.0} - (A_{510} - A_{700})_{\text{pH } 4.5}$ with a molar extinction coefficient of malvidin-3-glucoside of 28,000 L mol⁻¹ cm⁻¹. The results were expressed as mg of malvidin-3-glucoside equivalent per g fresh weight.

Total storage decay was assessed on the basis of the total decay after removing and weighing the healthy berries. The weight of the decayed berries was calculated by subtracting healthy berries from the total cluster weight. Thus, total decay was expressed as the percentage of decayed berries with respect to the original cluster weight.

2.3. Northern blot hybridization

Total RNA was extracted from the skin of grapes according to the method of Salzman et al. (1999). Samples of denatured total RNA (10 µg) were separated on 1.2% (w/v) agarose-formaldehyde gels. RNAs were transferred to Hybond-N membrane (USB, Amersham) using 20 × SSC and cross-linked using a UV Stratalinker 800 (Stratagene La Jolla, CA). Equal loading was confirmed by ethidium bromide staining and by membrane staining with methylene blue.

A partial cDNA clone of stilbene synthase was obtained by RT-PCR. cDNA synthesis was performed with 5 µg of total RNA from the skin of grapes treated with CO₂ and stored for 12 days at 0 °C. The reaction was carried out in the presence of 500 ng of oligo-dT with 100 units of reverse transcriptase (Ecogen). A stilbene synthase gene DNA fragment was obtained by PCR amplification using the cDNA as template and the combination of the sense primer 5'-CCAAACATTGGTGCTTATATGGCTC-3' and the anti-sense primer 5'-AGGGATTCTTTCTCATCTCATCCA-3'.

The PCR product was cloned into the pGEMT vector (Promega) and confirmed by sequencing.

The partial DNA probe was random-primer labelled with α³²P-dCTP. Filters were prehybridized and hybridized at 65 °C in 7% sodium dodecyl sulphate, 0.33 M phosphate buffer, pH 7.2, and 1 mM EDTA, then washed twice in 2 × SSC, 0.1% SDS at room temperature and twice in 0.1 × SSC, 0.1% SDS at 65 °C and exposed to Kodak X-Omat SX film at -80 °C. Autoradiographs were digitally scanned and band densities quantified by image densitometry using Scion Image software (Scion Corporation, Frederick, MD). The 100% was assigned to the maximum optical density value achieved in each Northern and the rest of the optical densities were normalized to the maximum value and expressed as percentage of relative accumulation (RA).

2.4. Laser analytical technique

Skin samples (0.5 g) homogenized in liquid nitrogen were extracted with 0.5 mL methanol at room temperature for 10 min with ultra-sonication for four times. The extracts were centrifuged, filtered and protected from light to avoid *cis*-isomerization of stilbenes. The experimental analysis of resveratrol from grape skin has already been described elsewhere (Montero et al., 2000, 2003; Orea et al., 2001), so only a brief description is given here. Essentially, it is based on the combination of laser desorption (LD) with resonance-enhanced multi-photon ionization (REMPI) coupled with time-of-flight mass spectrometry (TOF-MS) detection. It consists of two independent high vacuum chambers; the first chamber was used for both laser desorption and laser post-ionization of the sample followed by acceleration of the ions towards the second chamber, basically a time-of-flight unit with a twin-microchannel plate detector. The sample was deposited on a Pyrex disc, which was parallel to the first accelerating plate. A step motor was used to control disc rotation. The whole sample holder and motor assembly was attached to a linear translator to allow adjustment of the perpendicular direction to the desorption laser. This movement changes the rotation radius so as to increase the number of runs for a given sample.

First harmonic pulses of 5 ns duration from a Nd:YAG laser (1064 nm) were used for sample desorption, and a frequency-doubled dye laser was used to ionize the desorbed neutrals. A system for frequency-doubling the output of the dye laser and active wavelength laser scanning (INRAD-AT-III-UV) with a doubling crystal (BBO-TST) was used to scan the output from 235 up to 365 nm in search of the resonant wavelength of the target analyte. The wavelength used for analysis of trans-resveratrol was 302.1 nm, determined as the optimal wavelength for trans-resveratrol analysis in complex samples. The ions produced by the second laser pulse were accelerated towards the TOF tube by a Wiley-McLaren type acceleration system and detected by a twin-microchannel plate detector (Comstock CP-625C/50F) placed at the end of the TOF tube.

2.5. Statistical analyses

Data from at least three replicates per sample were subjected to analysis of variance (ANOVA) (Statgraphics program, STSC, Rockville, MD). Multiple variance analysis was employed to determine the significance of the data at $P \leq 0.05$.

3. Results

3.1. Changes in quality of bunches and in total decay in CO₂-treated and non-treated table grapes stored at 0 °C

As seen in Table 1 non-treated bunches presented a greater increase in the withering index at the end of low temperature storage than CO₂-treated bunches. With respect to the browning index of the rachis, an increase was observed in non-treated bunches while in CO₂-treated bunches the browning index was lower, indicating that CO₂ treatment was effective in maintaining the visual appearance of the rachis. Also, in non-treated bunches a significant decline in RWC was recorded under storage at low temperature in air. The decline in RWC was less in CO₂-treated fruit after 33 days. The beneficial effects of CO₂ treatment on increasing better appearance could be explained by the lower water loss of the rachis under this treatment. Moreover, CO₂-treated bunches lost less

Table 1

Withering index, browning index, relative water content (RWC), weight loss, dry matter (DM), soluble solids content (SSC), titratable acidity (TA), maturity index, pH, color parameters (L^* , a^* and C^*), total anthocyanins and total decay of grapes cv. Cardinal treated with 20% CO₂ and stored during 33 days at 0 °C

Quality parameters	After-harvest	33 days of storage at 0 °C	
		Non-treated	CO ₂ -treated
Withering index ^a	0	3.33	1.50
Browning index ^b	0	2.83	1.67
Relative water content (%)	88.78 a	56.52 b	76.97 ab
Weight loss (%)	0	7.42 a	3.93 b
Dry matter (%)	14.71 a	15.41 a	14.96 a
SSC (%)	12.85 a	14.10 b	14.28 b
TA (% tartaric acid)	0.84 a	0.69 b	0.77 c
Maturity index (SSC/TA)	15.24	20.23	18.43
pH	3.33 a	3.69 b	3.64 b
L^*	35.95 a	24.56 b	23.22 b
C^*	16.89 a	2.84 b	4.07 c
Total anthocyanins (mg g FW ⁻¹)	1.39 a	1.85 b	1.57 a
Total decay	0	25.50 a	5.00 b

^a Scale of withering: 0, none; 1, onset of withering in pedicel and apex of bunch; 2, withering of pedicel, apex of bunch and over 10% of the main stem; 3, withering in up to 50% of main stem; 4, total withering of main stem.

^b Scale of browning: 0, none; 1, slight; 2, moderate; 3, severe; 4, extreme. Means within files with different letters denotes statistically significant differences (LSD = 95%).

weight than did non-treated bunches. With respect to berry quality, we observed that at the end of low temperature storage, DM of CO₂-treated grapes did not change with respect to freshly harvested fruit, while a slight increase was recorded in non-treated grapes. SSC and TA at harvest were 12.85 and 0.843, respectively and the SSC/TA ratio was 15.24. This ratio increased in both non-treated and CO₂-treated fruit during cold storage, reaching values of 20.23 and 18.43, respectively. No major differences were observed for SSC between non-treated and CO₂-treated grapes after 33 days of storage. As regards the external colour of the berries, no browning occurred in CO₂-treated fruit. CO₂ treatment maintained the bright skin colour of harvested grapes better, with higher C^* value than non-treated grapes. The total content of the anthocyanins found at harvest was 1.39 mg g FW⁻¹ (Table 1). Both non-treated and CO₂-treated grapes exhibited an increase in total anthocyanins, but this increase was significantly higher in non-treated grapes. In CO₂-treated fruit the total decay incidence was significantly lower than in non-treated grapes (Table 1). After 33 days of storage at 0 °C, 25.5% of total decay was quantified in non-treated grapes, while 5.0% diseased berries were found in CO₂-treated clusters.

3.2. Effect of high CO₂ treatment on trans-resveratrol content during low temperature storage of grapes

Fig. 1 shows the change in the trans-resveratrol content in treated and non-treated samples obtained by LD+REMPI-TOFMS. In freshly harvested table grapes the trans-resveratrol content was 44.11 µg g FW⁻¹. While trans-resveratrol levels in CO₂-treated fruit showed a steady increase after 22 days at 0 °C, the non-treated grapes presented a sharp accumulation after 33 days of storage, reaching values of 69.89 µg g FW⁻¹. At this time, the trans-resveratrol content in the CO₂-treated grapes was only ca. 60% that of the non-treated grapes, with a value of 42.11 µg g FW⁻¹.

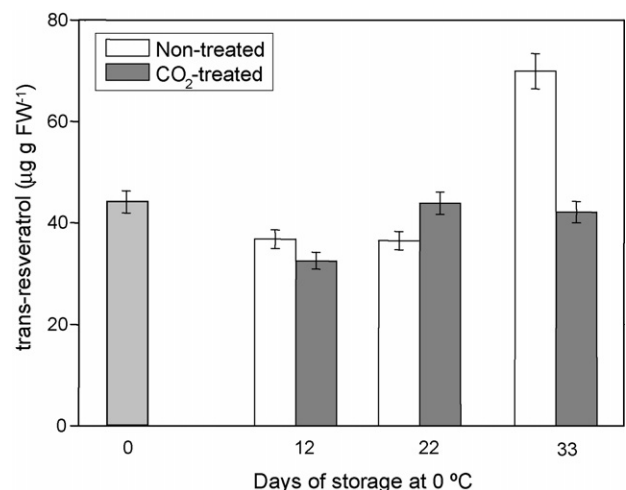


Fig. 1. Changes in trans-resveratrol content in the skin of CO₂-treated and non-treated 'cardinal' table grapes during 33 days of storage at 0 °C (see text for details). Values are the means of three replicate samples \pm S.E.

3.3. Effect of high CO₂ treatment on the accumulation of STS mRNA during low temperature storage of grapes

To determine whether low temperature storage may affect the pattern of *STS* gene expression in ‘cardinal’ grapes, and how low-temperature treatment with high CO₂ concentration affected transcript accumulation, the total mRNA prepared from the skin of CO₂-treated and non-treated grapes stored at 0 °C for up to 33 days was analyzed by Northern hybridization (Fig. 2). A partial cDNA clone of 773-bp of the stilbene synthase obtained by RT-PCR (GenBank Accession Number DQ235274) was used as a probe. The storage of grapes at 0 °C induced *STS* mRNA accumulation in both non-treated and CO₂-treated grapes. However, *STS* mRNA levels in the non-treated grapes were higher than in CO₂-treated fruit. In non-treated grapes there was a slow but progressive accumulation of *STS* transcript, which reached a maximum by day 28 and decreased slightly thereafter. However, the *STS* transcript in CO₂-treated grapes remained at stable low levels until the end of storage.

3.4. STS mRNA accumulation and trans-resveratrol content during the shelf-life of CO₂-treated and non-treated grapes at 20 °C

To simulate shelf-life during marketing of grapes, CO₂-treated and non-treated fruit stored for 33 days at 0 °C were transferred to 20 °C for 2 days and changes in the *STS* gene expression and trans-resveratrol content were analyzed. After 2 days at 20 °C, there was a sharp increase in the *STS* mRNA level in both treated and non-treated grapes, which was 35% greater in the non-treated fruit (Fig. 3). It is interesting to note that *STS* mRNA levels in CO₂-treated grapes did not increase during storage at 0 °C as occurred with non-treated grapes, where the accumulation of transcript was greater except for a decrease observed after 33 days of storage (Fig. 2). Upon transfer, the trans-resveratrol content was also higher in the skin tissues of non-treated grapes than in the treated ones. However, as noted earlier, at the beginning of this shelf-life

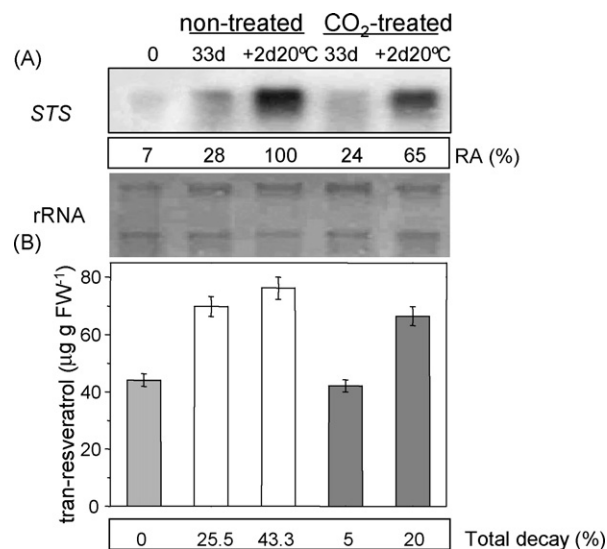


Fig. 3. Accumulation of *STS* mRNA (A) and trans-resveratrol (B) in the skin of CO₂-treated and non-treated Cardinal table grapes stored for 33 days at 0 °C and transferred to 20 °C for 2 days. (A) 10 µg of total RNA from the skin was fractionated by gel electrophoresis, blotted and hybridized with the *STS* probe. The intensity of the bands was quantified by scanning densitometry of the autoradiographs. Optical densities values were normalized to the maximum value and expressed as percentage of relative accumulation (RA). The equivalence of RNA loading of the lanes was demonstrated by methylene blue staining. (B) Trans-resveratrol values are the means of three replicate samples ± S.E.

period (after 33 days of storage), the trans-resveratrol content in the CO₂-treated grapes was only 55% of that observed in non-treated grapes. Thus, the trans-resveratrol increase rate during the shelf-life period was much more pronounced in the CO₂-treated samples: i.e., 72% versus only 10% in the non-treated samples. When table grapes were transferred to 20 °C for 2 days, although the levels of total decay increased sharply in both non-treated and CO₂-treated grapes, the increase rate was also much more pronounced in the CO₂-treated samples.

4. Discussion

During postharvest storage of table grapes serious problems arise from stem withering and browning which are detrimental to the visual appearance of the clusters and even determine table grape storability. A considerable deterioration in the visual appearance of non-treated clusters was observed after 33 days of storage at 0 °C (Table 1). The withering and browning indexes at the end of the storage were consistently lower in bunches pretreated with 20% CO₂ for 3 days than in non-treated bunches, with values of 1.50 and 3.33, respectively. On the other hand, high stem browning development has been reported after 2 months under CA treatments using CO₂ levels ≥ 15 kPa (Retamales et al., 2003). The beneficial effects of pretreatment of CO₂ on appearance of bunches could be explained by lower water loss from the rachis under this treatment. In the present work we analyzed the RWC of

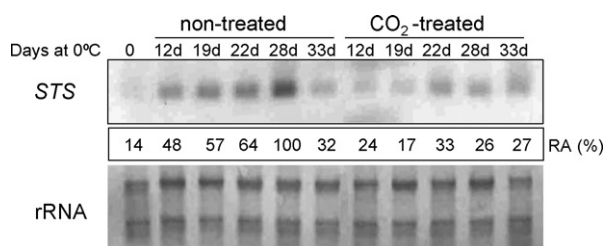


Fig. 2. Accumulation of *STS* mRNA in the skin of CO₂-treated and non-treated Cardinal table grapes stored for up to 33 days at 0 °C. 10 µg of total RNA from the skin was fractionated by gel electrophoresis, blotted and hybridized with the *STS* probe. The intensity of the bands was quantified by scanning densitometry of the autoradiographs. Optical densities values were normalized to the maximum value and expressed as percentage of relative accumulation (RA). The equivalence of RNA loading of the lanes was demonstrated by methylene blue staining.

the stem as an alternative measure of water status. The RWC is a measure of the actual water content relative to the water content at full turgidity, reflecting the metabolic activity in tissues (Flower and Lidlow, 1986). We observed that stem RWC in non-treated bunches declined sharply as a result of storage at 0 °C. In CO₂-treated stems, on the other hand, the lower increase in internal water content during rehydration could indicate an osmotic adjustment, which prevents perturbation of cell metabolism caused by low temperature. Also, many plant species during water stress conditions shows a decline in RWC (Nagy et al., 1995), including fruit tissues (Walter et al., 1990). The results showed that weight loss in CO₂-treated grapes was lower than in non-treated grapes after 33 days of storage (3.93 and 7.42, respectively, Table 1).

As regards berry quality, it is widely accepted that the most important parameters determining consumer acceptability of table grapes are bright red colour and the ratio between SSC and TA. No significant changes were observed for SSC between non-treated and CO₂-treated grapes after 33 days of storage, although SSC did increase significantly with respect to freshly harvested fruit. Since berries were collected at 12.85%, in an early harvest state, such an increase of soluble solids could be the result of normal postharvest metabolic activity. This accumulation was also reflected in the change in the SSC/TA ratio, which was lower in CO₂-treated fruit, indicating that this treatment delay the metabolic changes associated with maturation, so that development was less pronounced in CO₂-treated grapes than non-treated grapes. These results are consistent with previous work, which suggested that high CO₂ levels may act via physiological response of the fruit tissue to delay ripening and senescence of green tissues (Del Cura et al., 1996). It has been reported that in general, SSC, TA and pH values remained quite constant in several varieties of grapes stored at 0 °C under several Ca conditions (Crisosto et al., 2002; Artés-Hernández et al., 2006). Also, CO₂ treatment maintained berry skin colour better during cold storage, and no colour anomalies were found in CO₂-treated fruit; this is consistent with the findings of Cimino et al. (1987) in the white 'Italia' cultivar stored for 99 days at 0 °C under CA. With respect to the effect of pretreatment with high CO₂ levels on polyphenol compounds, we observed (Table 1) that at the end of the storage period the total anthocyanins content in the skin tissues was higher in non-treated than in CO₂-treated grapes.

A sharp rise in trans-resveratrol levels measured by REMPI-TOFMS took place in non-treated grapes after 33 days of storage at 0 °C. However no increase in trans-resveratrol content was observed in the skin tissues of CO₂-treated grapes. It has been reported that the content of trans-resveratrol in the skin of berries increased significantly in response to several stresses, such as O₃ shock, UV-C irradiation and pathogen infection (Creasy and Coffee, 1988; Sarig et al., 1997; Cantos et al., 2002). Our results show that at the end of the storage period, the highest trans-resveratrol content was detected in non-treated grapes, reaching values of 69.89 µg g FW⁻¹. In CO₂-treated grapes the trans-resveratrol

content was a ca. 60% that of non-treated grapes reaching values of 42.11 µg g FW⁻¹ (Fig. 1).

The differences observed between the CO₂-treated and non-treated grapes in trans-resveratrol levels were also observable in the levels of *STS* transcript (Fig. 2), demonstrating that inducible stilbene accumulation in skin berries is highly regulated at the level of *STS* gene expression. We have isolated a partial *STS* cDNA clone, and nucleotide and amino acid sequence analyses revealed that the encoded *STS* share significant levels of identity with *STS* sequences from *Vitis* (Melchior and Kindl, 1990; Wiese et al., 1994). *STS* mRNA levels in the non-treated grapes, which reached a maximum by day 28, were nonetheless substantially higher than in CO₂-treated fruit. It has been extensively studied that the expression of *STS* genes is induced in response to biotic and abiotic stresses such as pathogen infection (Preisig-Müller et al., 1999), ozone (Zinser et al., 2000) and UV-light (Versari et al., 2001). Pretreatment with high CO₂ levels appears to be a clear effect avoiding the induction of *STS* genes in CO₂-treated grapes during low temperature storage. In these treated grapes *STS* mRNA levels slightly increased and remained at stable state low levels until the end of storage. In a similar way, trans-resveratrol content in these CO₂-treated tissues remained virtually unchanged with respect to those quantified in freshly harvested grapes. Moreover, as we indicated above, no significant increase in total fungal decay was observed in CO₂-treated grapes (Table 1). After shelf-life at 20 °C, while trans-resveratrol content increased to 72% in CO₂-treated fruit, it only reached 10% in non-treated fruit. This high potentiality for synthesizing resveratrol in CO₂-treated grapes during shelf-life was similar to that of non-treated fruit at the end of storage at 0 °C. An increase has also been reported in resveratrol content (1.2 ± 0.6 µg g FW⁻¹ of grape samples at harvest) during shelf-life of table grapes stored under CA (Artés-Hernández et al., 2003). Our results suggest that *STS* gene expression and resveratrol accumulation are not associated with the reduction of fungal decay. Moreover, a further possible factor involved in this response is the early state of maturity of this red table grape variety. In this connection, a clear negative correlation has been reported between the resveratrol content of grape skin and the developmental stage of berries measured by the sugar concentration of the juice (Jeandet et al., 1995).

We conclude that the range of negative effects occurring in non-treated fruit stored at 0 °C, mostly increased withering and browning indices, water loss and total decay, were reduced by pretreatment with high CO₂ levels, thus improving the appearance of table grapes. Likewise, the CO₂ treatment consistently restrained the susceptibility of berries to total decay and the accumulation of *STS* mRNA and trans-resveratrol content. Our results indicate that the efficacy of high CO₂ pretreatment in reducing total fungal decay during low temperature storage is not mediated by induction of *STS* gene expression. Furthermore, these results point to new aspects of research aimed to identify responses in table grapes associated with low temperature storage and mechanism,

that confer a competitive advantage on CO₂-treated table grapes.

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ARTÍCULO 2

Involvement of the phenylpropanoid pathway in the response of table grapes to low temperature and high CO₂ levels.

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RESUMEN

Hemos analizado las respuestas inducidas por el almacenamiento a bajas temperaturas (0°C) en uva de mesa roja (*Vitis vinifera* cv. Cardinal) y también los efectos de un tratamiento con 3 días de altos niveles de CO₂ (20% CO₂ plus 20% O₂). A nivel transcripcional, hemos estudiado las enzimas clave de la ruta de los fenilpropanoides, L-fenilalanina amonio-liasa (PAL), chalcona sintasa (CHS) y estilbeno sintasa (STS), junto con los productos finales de algunas de estas enzimas, como el *trans*-resveratrol y antocianos totales, y su implicación en la capacidad antioxidante. Los resultados, usando cDNAs parciales previamente aislados, indicaron que el almacenamiento a 0°C durante 3 días aumentó los niveles de mRNA de *VcPAL*, *VcSTS* y *VcCHS* en la piel de uvas no tratadas, disminuyendo ligeramente en adelante. Por el contrario, la acumulación de estos transcritos fue menor en la piel de uva después de 3 días de tratamiento con CO₂, y fueron indetectables cuando la fruta tratada fue transferida a aire. Las bajas temperaturas modularon los niveles de antocianos totales y la capacidad antioxidante de uvas no tratadas, y redujeron el contenido de *trans*-resveratrol en uvas tratadas y no tratadas, aunque la disminución fue mayor en uvas tratadas con CO₂. El conjunto de estos resultados indicaron que las uvas tratadas con CO₂ podrían ser menos sensibles a cambios en la temperatura durante las primeras etapas de almacenamiento a 0°C, reduciendo los niveles de expresión de genes de la ruta de los fenilpropanoides y la acumulación de antocianos totales y capacidad antioxidante.



Involvement of the phenylpropanoid pathway in the response of table grapes to low temperature and high CO₂ levels

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Abstract

We have analyzed the responses induced by low temperature storage (0 °C) in red table grape (*Vitis vinifera* L. cv. Cardinal) and also the effect of a 3 day treatment of high CO₂ levels (20% CO₂ plus 20% O₂). At the transcriptional level we studied the key phenylpropanoid enzymes L-phenylalanine ammonia-lyase (PAL), chalcone synthase (CHS) and stilbene synthase (STS), together with the final products of some of these enzymes, such as *trans*-resveratrol and total anthocyanin, and their involvement in antioxidant activity. The results, using previously isolated partial cDNAs, indicated that storage at 0 °C for 3 days increased *VcPAL*, *VcSTS* and *VcCHS* mRNA levels in the skin of non-treated grapes, decreasing slightly thereafter. In contrast, the accumulation of these transcripts was lower in the skin of grapes after 3 days of CO₂ treatment, and was undetectable when treated fruit were transferred to air. Low temperature modulated total anthocyanin levels and antioxidant capacity in non-treated grapes, and reduced the *trans*-resveratrol content in both treated and non-treated grapes, although the decrease was higher in CO₂-treated grapes. The overall results indicated that CO₂-treated grapes could be less sensitive to temperature shifts during the first stages of storage at 0 °C, reducing the expression levels of phenylpropanoid genes and the accumulation of total anthocyanins and antioxidant activity.

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Keywords: Table grapes; Carbon dioxide; Phenylpropanoid pathway; Low temperature

1. Introduction

Table grape is a non-climateric fruit with significant quality losses during postharvest storage and marketing. These losses normally result from stem and pedicel desiccation, weight loss and softening of berries, and fungal decay, which is largely caused by *Botrytis cinerea*. The control of *B. cinerea* during storage and transportation is traditionally achieved by the application of SO₂ (Luvisi et al., 1992). Despite its efficacy, the use of SO₂ technology is restricted in most countries due to environmental and health concerns, justifying the search for alternatives. In the last decade, some alternative strategies, using modified atmosphere packaging (MAP) and controlled atmosphere (CA), have been tried in place of chemical treatments to control the development of decay (e.g., Crisosto et al., 2002;

Retamales et al., 2003; Artés-Hernández et al., 2006; Valero et al., 2006). In previous work, we have shown that high CO₂ pretreatment for 3 days reduced total decay in table grapes stored at 0 °C, thereby maintaining fruit quality (Romero et al., 2006a; Sanchez-Ballesta et al., 2006). The effectiveness of this pretreatment was not mediated by the induction of gene expression of stilbene and the pathogenesis-related protein (PRs) when the incidence of gray mold was evident in non-treated grapes (Romero et al., 2006a; Sanchez-Ballesta et al., 2006). There are no studies showing the effect of a 3 day CO₂ pretreatment in the first stages of grape storage at 0 °C on the modulation of defense responses before the appearance of natural decay. Such studies are needed to gain a complete understanding of the mechanisms involved in such a treatment.

Phenolic compounds are a group of important secondary plant metabolites which are implicated in fruit quality, affecting the appearance, taste and flavour of fruit, and grapes constitute one of the major sources of phenolic compounds among different fruit species (Macheix et al., 1990). Since phenolic compounds have also been shown to be implicated in plant

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resistance to different biotic and abiotic stresses (Dixon and Pavia, 1995), the study of their biosynthesis and regulation in fruit has attracted much attention. Phenylalanine ammonia-lyase (PAL; EC 4.3.1.5) catalyzes the first committed step in the phenylpropanoid pathway, which produces a variety of phenolic compounds with structural and defense-related functions, including anthocyanins, flavonoid pigments, furanocoumarins, phytoalexins, lignin and wound phenolic esters (Hahlbrock and Scheel, 1989; Dixon and Pavia, 1995). Phytoalexins from *Vitis* species seem to constitute a rather restricted group of molecules belonging to the stilbene family (Langcake and Pryce, 1977), the skeleton of which is based on the *trans*-resveratrol structure. *Trans*-resveratrol synthesis is catalyzed by stilbene synthase (STS), which is closely related to chalcone synthase (CHS), the key enzyme of flavonoid-type compounds like anthocyanins. Both enzymes catalyze common condensation reactions of 4-coumaroyl-CoA with three malonyl-CoA units but with different cyclization reactions.

The activation of phenylpropanoid metabolism may play a role in the development of protective barriers in stress-damaged cells. For example, transgenic plants with suppressed levels of PAL exhibit spontaneous necrosis (Tamagnone et al., 1998), or more rapid and extensive lesion development than do wild-type plants after pathogen infection (Maher et al., 1994), suggesting that inhibition of phenylpropanoid biosynthesis might compromise plant health. The accumulation of *PAL*, *STS* and *CHS* mRNAs has been described in response to biotic and abiotic stresses (Leyva et al., 1995; Gläbgen et al., 1998; Brehm et al., 1999; Preisig-Müller et al., 1999; Sanchez-Ballesta et al., 2000; Franca et al., 2001; Versari et al., 2001). The coordinated accumulation of *PAL* and *CHS* mRNAs suggests that their response to such diverse stimuli may be regulated through a common controlling mechanism (Loake et al., 1991).

The aim of the present work was to analyze phenylpropanoid gene expression in red table grapes as a marker for changes in response to low temperature (0 °C) after harvest, and also to assess how the table grapes respond to high CO₂ levels (20%) at 0 °C at the end of the pretreatment and when grapes are transferred to air before the appearance of decay. To this end we analyzed different key phenylpropanoid enzymes (*PAL*, *STS*, *CHS*) at the transcriptional level. We also assessed levels of the final products of the action of some of these enzymes, such as *trans*-resveratrol and total anthocyanin, and examined their implication in the antioxidant activity of the skin of treated and non-treated grapes.

2. Materials and methods

2.1. Plant material

Table grapes (*Vitis vinifera* L. cv. Cardinal) were harvested at random in Camas (Sevilla, Spain) in July 2003 (12.85% total soluble solids and 0.84% tartaric acid). After harvesting, field-packaged bunches were transported to the laboratory, where fruit were immediately forced-air precooled for 14 h at −1 °C. After cooling, the bunches free from physical and pathological defects were randomly divided into two lots and stored at 0 ± 0.5 °C and

95% relative humidity (RH) in two sealed neoprene containers of 1 m³ capacity. Ten plastic boxes containing about 3 kg of table grapes per box were stored in each container in the dark. One lot was stored under normal atmosphere (non-treated fruit) and the other under a gas mixture containing 20% CO₂ + 20% O₂ + 60% N₂ (CO₂-treated fruit) for 3 days. After 3 days, CO₂-treated grapes were transferred to air under the same conditions as non-treated fruit for up to 6 days at 0 °C. Ten clusters were sampled after cooling at −1 °C (pre-stored grapes, 0 days) and after 3 and 6 days of storage at 0 °C, and berries from five clusters (approximately 300 g each cluster) were peeled and the skin and pulp were frozen in liquid nitrogen, ground to a fine powder and stored at −80 °C until analysis. For analysis of quality parameters, 45 berries were randomly removed from five clusters and distributed in three replicates of 15 berries each.

2.2. Quality assessments

Berry quality assessment comprised soluble solids contents (SSC), pH, titratable acidity (TA) and colour. SSC was determined using a digital refractometer Atago PR-101 (Atago Co. Ltd., Japan) at 20 °C and expressed as a percentage. The pH of the juice was measured in a pH meter with a glass electrode. TA was determined by titration with 0.1N NaOH up to pH 8.1 and results were expressed as % tartaric acid.

Berry skin colour was measured at three different positions around the equatorial region using the Hunter Lab System and a Minolta CR200TM colorimeter (Minolta Camera Co., Osaka, Japan). Results were given in Commission Internationale de l'Eclairage *L*^{*} (lightness), *a*^{*}, and *b*^{*} (CIELAB) colour space coordinates. Hue (*h*[°]) ($\tan^{-1} b/a$) and chroma (*C*^{*}, saturation) [$(a^2 + b^2)^{1/2}$] were calculated from *a*^{*} and *b*^{*}.

For flesh and skin firmness, grapes were tested on an Instron model 4501 (High Wycombe, UK) fitted with different cylindrical, flat-surfaced plungers, depending on the mechanical test. Skin rupture force was measured on the equatorial side of the berry using a 1 mm diameter plunger, and was determined by measuring the peak force required for the probe to penetrate the skin. Compressive firmness was measured separately on berries of approximately similar size, as the force required to compress the berry using a 35-mm diameter plunger and full-scale load of 100 N at a crosshead speed of 50 mm min^{−1}, until the berry began to release juice. Firmness was expressed in newtons (N).

2.3. Northern blot hybridization

Total RNA was extracted from the skin and pulp of grapes according to the method of Salzman et al. (1999). Samples of denatured total RNA (10 µg) were separated on 1.2% (w/v) agarose-formaldehyde gels. RNAs were transferred to Hybond-N membrane (USB, Amersham) using 20× SSC and cross-linked using a UV Stratalinker 800 (Stratagene La Jolla, CA). Equal loading was confirmed by ethidium bromide staining and by membrane staining with methylene blue.

As probes we used *PAL* (GenBank accession no. DQ887093), *CHS* (GenBank accession no. DQ887094) and *STS* (GenBank no. DQ235274) partial DNAs, previously isolated (Sanchez-

Ballesta et al., 2006; Romero et al., 2007). Probes were random-primer labelled with $\alpha^{32}\text{P}$ -dCTP. Filters were prehybridized and hybridized at 65 °C in 7% sodium dodecyl sulphate, 0.33M phosphate buffer, pH 7.2, and 1 mM EDTA, then washed twice in 2× SSC, 0.1% SDS at room temperature and twice in 0.1× SSC, 0.1% SDS at 65 °C and then exposed to Kodak X-Omat SX film at −80 °C. Autoradiographs were digitally scanned and band densities quantified by image densitometry using Scion Image software (Scion Corporation, Frederick, MD). A value of 100% was assigned to the maximum optical density value achieved in each northern blot and the rest of optical densities were normalized to the maximum value and expressed as percentage of relative accumulation (RA).

2.4. Resveratrol content: laser analytical technique

Skin samples (0.5 g) homogenized in liquid nitrogen were extracted four times with 0.5 mL methanol at room temperature for 10 min with ultra-sonication. The extracts were centrifuged, filtered and protected from light to avoid *cis*-isomerization of stilbenes. The resveratrol content was measured as described by Orea et al. (2001) based on the combination of laser desorption (LD) with resonance-enhanced multi-photon ionization (REMPI) coupled with time-of-flight mass spectrometry (TOF-MS) detection. The results were expressed as microgram per gram fresh weight.

2.5. Analysis of total anthocyanin content

Total anthocyanin content was determined by the pH differential method as reported by Wrolstad (1976). Briefly, skin samples (0.5 g) homogenized in liquid nitrogen were extracted with 0.01% HCl in 0.5 mL methanol using ultra-sonication with cold water, four times for 10 min each. The extracts were centrifuged and the supernatants were removed and filtered. Absorbance was measured in a UV–vis spectrophotometer (UV-VIS 1601 Shimadzu) at 510 nm and at 700 nm in buffers at pH 1.0 and 4.5 using $A = [(A_{510} - A_{700})_{\text{pH}1.0} - (A_{510} - A_{700})_{\text{pH}4.5}]$ with a molar extinction coefficient of malvidin-3-glucoside of 28,000 L mol^{−1} cm^{−1}. The results were expressed as mg of malvidin-3-glucoside equivalents per gram fresh weight.

2.6. Radical cation ABTS scavenging capacity

Extraction of skin samples was performed in the same way as anthocyanin extraction described above. The radical cation 2,2'-azinobis(3-ethylbenzothiazoline 6-sulphonate) (ABTS⁺) scavenging capacity was measured as described by Rice-Evans et al. (1996), where ABTS⁺ is oxidized with potassium persulfate. Trolox (Hoffman-La Roche) (6-hydroxy 2,5,7,8-tetramethylchroman-2-carboxylic acid) (2.5 mM) prepared in ethanol was used as an antioxidant standard and for the calculation of scavenging capacity of grape skin extracts as trolox equivalent. The scavenging activity of grape skin extracts was calculated as millimolar TE per gram sample.

2.7. Statistical analyses

Experimental data are the mean ± S.E. of three replicate samples of the determination for each sample. A variance analysis (one-way ANOVA) using the Fisher's least significant difference (LSD) test (Statgraphics 5.1 Plus program, STSC, Rockville, MD) was performed to determine if the *trans*-resveratrol, total anthocyanin content and antioxidant activity induced in CO₂-treated and non-treated grapes stored at 0 °C showed significant differences ($P \leq 0.05$).

3. Results

3.1. Quality of bunches of table grapes stored at 0 °C at the end of CO₂ treatment and after transferring to air

Storage at 0 °C for 3 days increased the SSC content in non-treated grapes, whereas in the 3 day CO₂-treated grapes the increase was smaller. The CO₂ treatment also restrained the decrease in TA values observed in non-treated grapes after 3 days. The pH of non-treated grapes increased after 3 days at 0 °C, but this increase was smaller in 3 day CO₂-treated ones (Table 1). At 0 °C, when 3 day-treated grapes were transferred to air the SSC, TA and pH values were similar to those observed in non-treated grapes. The external colour of the berries showed no browning in CO₂-treated fruit, and there were no significant differences between the L^* , C^* and Hue values of treated and non-treated grapes stored for 6 days at 0 °C. The combination of storage at 0 °C and CO₂ treatment did not affect skin toughness or fruit firmness compared to storage at 0 °C in air, and there were no significant differences in the puncture and compressive forces. After 6 days at 0 °C, both treated and non-treated grapes did not show any total decay (data not shown).

3.2. Phenylpropanoid gene expression in table grapes stored at 0 °C at the end of CO₂ treatment and after transfer to air

To investigate whether storage at low temperature and/or 3 days of high CO₂ treatment may modulate the pattern of phenylpropanoid gene expression in grapes, total mRNA prepared from the skin and pulp of CO₂-treated and non-treated grapes stored at 0 °C was analyzed by northern hybridization (Fig. 1).

The partial *VcPAL*, *VcSTS* and *VcCHS* probes were previously isolated (Sanchez-Ballesta et al., 2006; Romero et al., 2007). The deduced PAL amino acid sequence showed 35% identity with a *V. vinifera* PAL sequence from the cultivar 'Cabernet Sauvignon' (GenBank accession no. BAA31258) and 92% identity with a PAL from 'Lambrusco' (GenBank accession no. X75967). Comparison of the partial deduced CHS and STS amino acid sequences revealed that they were highly homologous (>90% identity) to different CHS and STS sequences from *V. vinifera*. Northern analysis revealed no *PAL*, *STS* and *CHS* gene expression in the pulp. Storage of grapes at 0 °C induced accumulation of *PAL*, *STS* and *CHS* in the skin of non-treated grapes after 3 days, decreasing slightly after 6 days (Fig. 1). In the skin of 3 day CO₂-treated grapes the increase in the

Table 1
Total soluble solids content (SSC), titratable acidity (TA), pH, colour parameters (L^* , C^* and hue), compressive and puncture firmness of grapes cv. Cardinal treated with 20% CO₂ and stored for up to 6 days at 0 °C

Quality parameters	0 day	3 day air 0 °C	3 day CO ₂ 0 °C	6 day air 0 °C	3 day CO ₂ + 3 day air 0 °C
SSC (%)	12.85a	14.66c	13.23a	14.55c	13.75b
TA (% tartaric acid)	0.843c	0.74a	0.82c	0.8b	0.79b
pH	3.33a	3.58d	3.49c	3.44b	3.44b
L^*	36.16a	34.63a	36.48a	32.54a	33.27a
C^*	13.48a	10.03a	10.1a	9.54a	9.58a
Hue (angle)	349a	345a	345a	350a	363a
Compressive firmness (N)	21.18a	19.15a	19.15a	19.54a	18.76a
Puncture firmness (N)	0.89a	0.89a	0.95a	0.91a	0.81a

Mean in the same row with different letters (a–d) denote a statistically significant differences (LSD = 95%).

accumulation of these transcripts was lower and was practically undetectable after 6 days of cold storage.

3.3. Accumulation of *trans*-resveratrol, total anthocyanin and antioxidant activity in table grapes stored at 0 °C at the end of CO₂ treatment and after transfer to air

The *trans*-resveratrol content decreased significantly in the skin of non-treated grapes after 3 days at 0 °C. As occurred with *STS* gene expression, the 3 day CO₂ treatment reduced the resveratrol content 1.7 times more than in non-treated grapes stored at 0 °C. The reduction of resveratrol content induced by high CO₂ levels was also maintained when treated fruit were transferred to air at 0 °C, with values 1.5 times lower than in non-treated grapes (Fig. 2).

Total anthocyanin levels were 1.63 times greater in non-treated grapes after 3 days of storage at 0 °C than in pre-stored

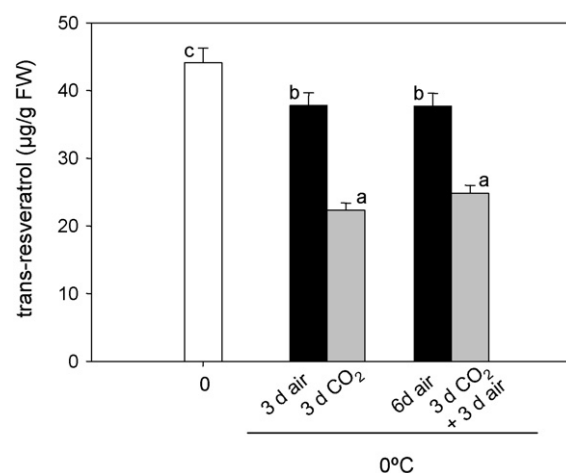


Fig. 2. Changes in *trans*-resveratrol content in the skin of non-treated and CO₂-treated table grapes cv. Cardinal stored at 0 °C. Values are the means of three replicates ± S.E. Values labeled with the same letter are not different at the 5% significance level.

grapes (0 days), whereas they were only 1.2 times higher in 3 day CO₂-treated grapes. However, when treated fruit were transferred to air at 0 °C, anthocyanin levels were significantly higher than in non-treated grapes stored for 6 days at 0 °C (Fig. 3A).

Antioxidant activity of the skin of pre-stored grapes (0 days) was 25 mM TE/g of FW. Whereas in non-treated grapes stored at 0 °C for 3 days antioxidant activity was 1.1 times higher than in pre-stored grapes, in 3 day CO₂-treated grapes the antioxidant activity decreased, reaching values 1.5 times lower than in non-treated fruit (Fig. 3B). After 6 days of storage at 0 °C, antioxidant activity significantly increased in non-treated grapes whereas similar values were quantified in 3 day CO₂-treated fruit transferred to air.

4. Discussion

It is widely accepted that low temperature storage is one of the most effective technologies to extend postharvest life, but there are no references to studies on the responses of table grapes to the first stage at low temperature. SSC and TA are important quality factors determining table grape acceptability to consumers. In general, it has been reported that SSC, TA and pH values remain fairly constant in different grape varieties dur-

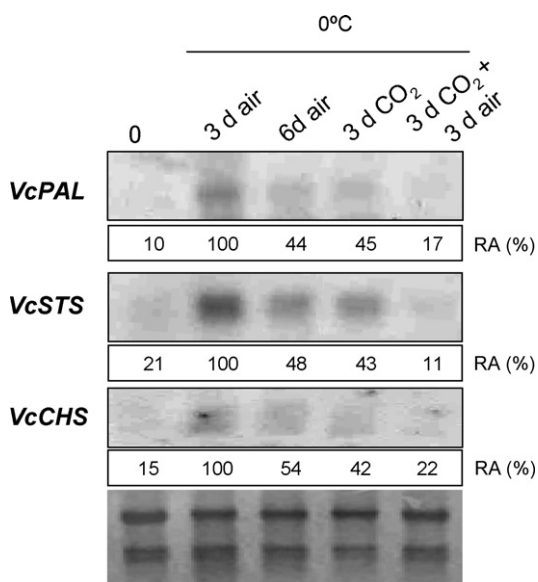


Fig. 1. Effect of high CO₂ pretreatment on *VcPAL*, *VcSTS* and *VcCHS* mRNA accumulation in the skin of table grapes cv. Cardinal stored at 0 °C. Ten micrograms of total RNA from the skin was fractionated by gel electrophoresis, blotted and hybridized with the partial probes. The intensity of the bands was quantified by scanning densitometry of the autoradiographs. Optical densities values were normalized to the maximum value and expressed as percentage of relative accumulation (RA). The equivalence of RNA loading of the lanes was demonstrated by methylene blue staining.

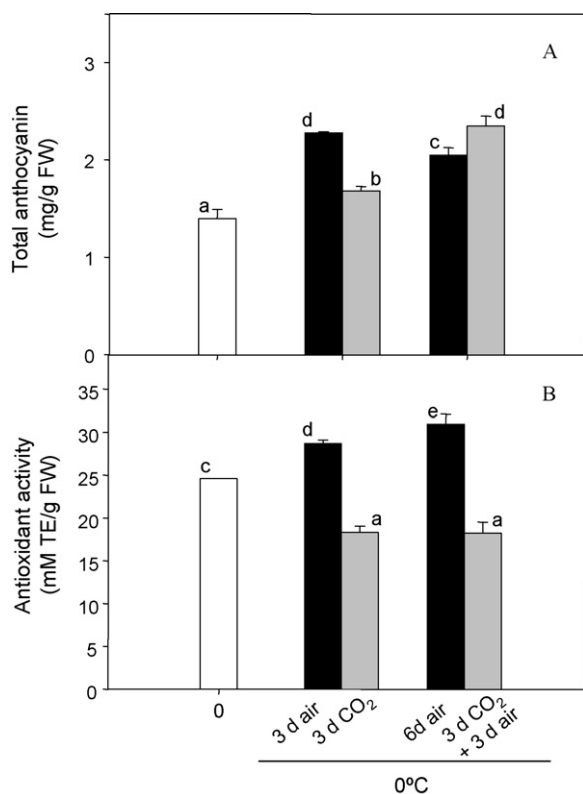


Fig. 3. Changes in total anthocyanin levels (A) and antioxidant activity (B) of non-treated and CO₂-treated table grapes cv. Cardinal stored at 0 °C. Values are the means of three replicates \pm S.E. Values labeled with the same letter are not different at the 5% significance level.

ing long-term cold storage under different high CO₂ conditions (Crisosto et al., 2002; Artés-Hernández et al., 2006; Sanchez-Ballesta et al., 2006). The application of CO₂ pretreatment for 3 days at 0 °C, caused a slight increase in SSC and pH compared to those observed in pre-stored fruit. In non-treated fruit, storage at low temperature for 3 days caused a more important increase in the SSC and pH values and a decrease in TA (Table 1). After 6 days of storage, however, these differences in the quality parameters of treated and non-treated grapes were less marked. In 'Flame' table grapes, Martínez-Romero et al. (2003) observed an increase in the SSC content of about 2.5 °Brix after 4 days at 1 °C, which was about 1 °Brix when grapes were stored under MAP conditions. On the other hand, no significant changes were observed in skin colour parameters or fruit firmness between treated and non-treated grapes stored at 0 °C for up to 6 days (Table 1).

Storage for 3 days at 0 °C sharply increased the abundance of *PAL*, *STS* and *CHS* transcripts in the skin of non-treated grapes, decreasing slightly after 6 days (Fig. 1). This increase in mRNA levels in response to low temperature storage was lower after 3 days of CO₂ treatment at 0 °C and undetectable when treated fruit were transferred to air at the same temperature (Fig. 1). In photosynthetically active tissue, such as leaves of chilling tolerant *Arabidopsis thaliana*, *PAL* and *CHS* mRNA accumulate at low temperature in a light-dependent manner (Leyva et al., 1995). In the case of fruit, whereas the increase in apple *PAL* activity in response to different storage temperatures has been

shown to be light dependent (Tan, 1980), in citrus tissues induction of *PAL* transcription and *PAL* activity is light independent (Sanchez-Ballesta et al., 2000). Our results in darkness indicate that a low temperature, such as 0 °C can by itself induce this phenylpropanoid gene expression in grapes. Although *V. vinifera* is tolerant to chilling, this activation of phenylpropanoid gene expression in the first stage of storage could be related to the perception by the fruit of a change in temperature, which could be less noticeable in CO₂-treated grapes. Christie et al. (1994) reported that the genes of the anthocyanin biosynthetic pathway, such as *PAL* and *CHS* can be considered 'cor' (Cold-Regulation) genes. The differences observed in phenylpropanoid gene expression between CO₂-treated and non-treated grapes could be consequence of a different perception of temperature shift. In this respect, an increasing number of studies have shown the existence of cross-adaptation in plants, so that exposure to a moderate stress not only induces resistance to this kind of severe stress but can also improve tolerance to other stresses (Bowler and Fluhr, 2000; Wang et al., 2003). In consequence, the application of high CO₂ levels (20%) in table grapes might improve tolerance to temperature shift.

Expression of *STS* genes is often induced in response to biotic and abiotic stresses, such as pathogen infection (Preisig-Müller et al., 1999), ozone (Brehm et al., 1999) and UV-light (Versari et al., 2001). To our knowledge, however, this is the first study showing regulation of *STS* gene expression by a temperature as low as 0 °C in grapes. The fact that after storage at 0 °C, the *STS* mRNA levels increased in treated and non-treated grapes while *trans*-resveratrol content decreased could indicate that low temperature affects post-transcriptional events. Furthermore, it is possible that the decrease was the result of subsequent oxidative coupling of *trans*-resveratrol producing several oligomers, such as ϵ and α -viniferins (Langcake and Pryce, 1977). In *Rehmannia glutinosa*, a perennial medicinal plant, resveratrol content has been found to decrease under low temperature (15 °C) treatment (Chung et al., 2006). Nevertheless, the fact that the reduction of *trans*-resveratrol content was greater in CO₂-treated than in non-treated grapes indicates a specific fruit response to low temperature and a different metabolic situation in the CO₂-treated grapes.

The induction of *PAL* and *CHS* mRNA accumulation was accompanied by an increase in total anthocyanin content, except in the case of 3 days CO₂ + 3 days air (Fig. 3A). In red 'Cardinal' grapes, a sharp increase in total anthocyanin content was observed in non-treated grapes after 3 days at 0 °C, decreasing thereafter. It is already known that anthocyanin synthesis continues after harvest and also during long-term cold storage. Mori et al. (2005) demonstrated that low night temperatures markedly increased anthocyanin synthesis in grape berries through the regulation of *PAL* activity and *CHS* gene expression. Veazie and Collins (2002) reported that total monomeric anthocyanin in 'Navaho' blackberries held in CA storage at 2 °C increased in the first 3 days and decreased thereafter. In contrast, high CO₂ applied as CA or MAP inhibited the postharvest increase of anthocyanin concentrations in strawberries and cherries (Gil et al., 1997; Remon et al., 2004). However, in 3 day CO₂-treated grapes the increase in total anthocyanin was significantly

smaller; they increased when grapes were transferred to air, reaching values similar to those observed in non-treated grapes after 3 days. In both cases, the increase in total anthocyanin levels was not accompanied by changes in the colour parameters measured, such as L^* , C^* and hue angle, which remained similar to those observed in pre-stored grapes.

The increase of total anthocyanin content in non-treated grapes was paralleled by an increase in antioxidant activity during low temperature storage (Fig. 3A and B). By contrast, while total anthocyanin content increased slightly in CO₂-treated grapes, there was a sharp decrease in antioxidant activity. Environmental stresses, such as low temperature induce free radicals in plants, and antioxidant activity has been found to be as much as 1.77 times higher in tomatoes stored at 5 °C than in those stored at 12 °C (Javanmardi and Kubota, 2006). Likewise, biotic and abiotic stresses increase phenolic metabolism and antioxidant capacity in spinach (Howard et al., 2002). On the other hand, no changes in antioxidant activity were detected in apples stored at low temperature under CA conditions (van der Sluis et al., 2001), but there was a decrease in antioxidant activity of samples of fresh-cut spinach stored at 10 °C under MAP (Gil et al., 1999).

The overall results suggest that table grapes, classified as chilling tolerant fruit, could be sensitive to temperature shifts during the first stage of storage at 0 °C. In non-treated grapes phenylpropanoid gene expression, total anthocyanin accumulation and antioxidant activity are activated, whereas the application of high CO₂ treatment reduces these responses. Likewise, the fact that the accumulation of some defense compounds like resveratrol was lower in CO₂-treated grapes could indicate that this treatment results in the activation of mechanisms to induce resistance in table grapes stored at low temperature. However, further analyses are needed to identify mechanisms associated to the response of table grapes to 0 °C in the first stage of storage and to determine whether high CO₂ levels could modulate them.

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ARTÍCULO 3

Anthocyanin, antioxidant activity and stress-induced gene expression in high CO₂-treated table grapes stored at low temperature.

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RESUMEN

Un pretratamiento con 20 kPa CO₂+20 kPa O₂+60 kPa N₂ durante 3 días fue efectivo en mantener la calidad de la fruta y controlar el ataque por hongo de uvas de mesa (*Vitis vinifera* cv.Cardinal) almacenadas a 0°C. En este trabajo, analizamos si el contenido en antocianos totales, el mecanismo molecular implicado en su biosíntesis y la actividad antioxidante está relacionado con el efecto beneficioso de este tratamiento gaseoso. Aislamos cDNAs parciales que codifican para enzimas implicadas en la biosíntesis de antocianos tales como L-fenilalanina amonio-liasa (PAL) y chalcona sintasa (CHS) y una enzima antioxidante como la ascorbato peroxidasa (APX). Las bajas temperaturas indujeron una acumulación de antocianos totales en la piel de uvas tratadas y no tratadas, aunque los niveles fueron menores en fruta tratada con CO₂. Por el contrario, la actividad antioxidante decreció durante el almacenamiento a 0°C en uvas no tratadas pero no cambió en uvas tratadas con CO₂. El aumento en los niveles de expresión de los genes asociados a la biosíntesis de antocianos y del mRNA *VcAPX* observado en uvas no tratadas, no se observó en uvas tratadas con CO₂, las cuales presentaron bajos niveles de ataque por hongo. Estos resultados señalan la habilidad de las uvas tratadas con CO₂ para prevenir la generación de especies reactivas de oxígeno más que su inactivación por medio de la inducción de los sistemas de defensa estudiados.



Anthocyanin, antioxidant activity and stress-induced gene expression in high CO₂-treated table grapes stored at low temperature

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KEYWORDS

Anthocyanin
biosynthesis;
Ascorbate
peroxidase;
Carbon dioxide;
Gene expression;
Table grapes

Summary

A pretreatment with 20 kPa CO₂+20 kPa O₂+60 kPa N₂ for 3 days proved effective in maintaining the fruit quality and controlling decay in table grapes (*Vitis vinifera* cv. Cardinal) stored at 0 °C. In the present work, we analyzed whether total anthocyanin content, the molecular mechanism implicated in their biosynthesis and antioxidant activity is related to the beneficial effect of this gaseous treatment. We isolated partial cDNAs that codified for enzymes implicated in the anthocyanin biosynthesis such as L-phenylalanine ammonia-lyase (PAL) and chalcone synthase (CHS), and an antioxidant enzyme such as ascorbate peroxidase (APX). Low temperatures induced an accumulation of total anthocyanin content in the skin of both treated and non-treated grapes, although levels were lower in CO₂-treated fruit. By contrast, antioxidant activity decreased during storage at 0 °C in non-treated grapes but did not change in CO₂-treated grapes. The up-regulation of anthocyanin biosynthesis gene expression and VcAPX mRNA observed in non-treated grape is not enhanced in CO₂-treated grapes, which presented low total decay. These results point out the ability of CO₂-treated grapes to prevent the generation of reactive oxygen species rather than their inactivation by means of induction of studied defense systems.

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Abbreviations: APX, ascorbate peroxidase; CA, controlled atmosphere; CHS, chalcone synthase; FW, fresh weight; MAP, modified atmosphere packaging; PAL, L-phenylalanine ammonia-lyase; ROS, reactive oxygen species; TE, equivalent of trolox

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Introduction

One of the main goals of postharvest technology in table grapes is to delay fungal attack, mainly caused by *Botrytis cinerea*, which causes extensive

losses during cold storage. The possibility of safe alternative control methods to assure high-quality fruit and control fungal attack is really important because postharvest chemical treatments are restricted in most countries. Among the alternative methods for controlling table grapes postharvest decay, such as modified atmosphere packaging (MAP) (Artés-Hernández et al., 2006) and controlled atmosphere (CA) (Yahia et al., 1983; Crisosto et al., 2002), high CO₂ pretreatment for shorter storage periods during postharvest handling of table grapes offers interesting possibilities. In previous works, we reported that pretreatment with 20% CO₂ and 20% O₂ for 3 days reduced fungal decay in table grapes stored at 0 °C while maintaining the fruit quality (Romero et al., 2006; Sanchez-Ballesta et al., 2006). The 3-day high CO₂ pretreatment also reduced rachis browning, which is a limitation on prolonged CA storage (Crisosto et al., 2002; Retamales et al., 2003). However, little is known about the physiological and molecular events occurring in response to the application of high CO₂ levels in table grapes. Our previous studies indicated that the efficacy of high CO₂ pretreatment is not mediated by the induction of pathogenesis-related proteins such as class I chitinase and β -1,3-glucanase (Romero et al., 2006). Moreover, the stilbene phytoalexin biosynthesis in CO₂-treated fruit was not induced (Sanchez-Ballesta et al., 2006). Stilbene synthase (STS), the enzyme leading to stilbene synthesis, is closely related to chalcone synthase (CHS), the enzyme implicated in the biosynthesis of flavonoid-type compounds like anthocyanins. CHS and STS catalyze common condensation reactions of *p*-coumaroyl-CoA and three C(2)-units from malonyl-CoA but different cyclization reactions to produce naringenin chalcone and resveratrol, respectively. Owing to the fact that the development of protection strategies of CO₂-treated grapes is not based on the induction of STS gene expression and resveratrol accumulation, this work focuses on the effect of high CO₂ levels on anthocyanin biosynthesis.

Anthocyanins, the main pigments in flowers and fruits, are a flavonoid subclass synthesized from hexose through the shikimate, phenylpropanoid and flavonoid pathways. The anthocyanin biosynthetic pathway is one of the well-known pathways in plants (Holton and Cornish, 1995). The first committed step is catalyzed by CHS, which condenses the metabolites malonyl-CoA and 4-coumaroyl-CoA formed essentially via the shikimate and/or malonate pathways. It has been suggested that anthocyanins function as photoprotective pigments (Li et al., 1993), and anthocyanin accumulation can reportedly be induced in many plants by biotic and

abiotic stresses, such as UV-B radiation, pathogen attack or low temperature (Mancinelli, 1983; Winkel-Shirley, 2001). In view of these findings, it is possible that the efficacy of high CO₂ pretreatment in preventing fungal attack was related with the effect on the synthesis of such protective phenolic compounds. Most studies of table grapes treated with CO₂ have addressed the quantity and type of anthocyanins, but there is still a dearth of knowledge about the expression of the anthocyanin biosynthetic genes in relation to these beneficial postharvest treatments.

Phenylalanine ammonia-lyase (PAL; EC 4.3.1.5) is the enzyme at the entry-point of the phenylpropanoid pathway, which yields a variety of phenolic compounds with structural and defense-related functions. PAL catalyzes the deamination of L-phenylalanine to form *trans*-cinnamic acid, which eventually leads to the production of *p*-coumaroyl-CoA the common substrate of STS and CHS. Owing to the nature and function of the products derived from the phenylpropanoid pathway, PAL activity and the activation of PAL under stress conditions have been considered part of a defense mechanism operating in stress-afflicted cells (Dixon and Pavia, 1995). Therefore, molecular analysis of PAL was also chosen as a mean to understand the effect of high CO₂ levels on table grapes stored at low temperatures.

Production of reactive oxygen species (ROS) during so-called “oxidative burst” is thought to be a central event in activation of disease resistance. In plant cells, the enhanced generation of ROS in response to both abiotic and biotic constraints has been well documented (Mehdy et al., 1996; Alscher et al., 1997). However, it is not clear whether changes in ROS generation are directly involved in the activation of plant defense response or are a mere consequence of the oxidative stress occurring in the attacked cells. Oxidative events are associated with the different *B. cinerea*-plant interactions, but their precise role in such interactions remains unclear (Grovin and Levine, 2000; Tierens et al., 2002). Hydrogen peroxide (H₂O₂) represents a crucial crossing in the mechanisms of oxidative stress, and its regulation plays an important role in cell life. Therefore, different systems are utilized by cell to balance the levels of H₂O₂. Ascorbate peroxidases (APX) (EC 1.11.1.11) utilize ascorbic acid and its specific electron to reduce H₂O₂ to water. APX genes have been isolated from some plants and their expression has been determined under fruit ripening, oxidative stress and low temperature, respectively (Kim and Chung, 1998; Yoshimura et al., 2000; Kawakami et al., 2002). In grape, there have been

no reports on the involvement of APX in *Botrytis* attack or on the effect of a beneficial high CO₂ pretreatment in controlling decay; we therefore isolated an APX partial cDNA and analyzed the changes in gene expression in treated and non-treated table grapes stored at low temperatures.

In order to further our knowledge of the mode of action of high CO₂ pretreatment, we have analyzed total anthocyanin content and antioxidant capacity as they relate to the beneficial effect of the gaseous treatment. Considering the role of PAL and CHS in the anthocyanin biosynthesis, we have cloned a *VcCHS* and *VcPAL* partial cDNA clones and monitored their expression in treated and non-treated grapes during low-temperature storage. This paper also reports our findings on the relationship between APX regulation at transcript level and susceptibility to development of natural fungal decay at low temperature.

Materials and methods

Plant material

Table grapes (*Vitis vinifera* L. cv. 'Cardinal') were harvested at random in Camas (Sevilla, Spain) in July. Early-harvesting mature berries were used in this work (12.85% total soluble solids; 0.84% tartaric acid). After harvesting, field-packaged bunches were transported to the laboratory, where fruits were immediately forced-air precooled for 14 h at -1°C . After cooling, bunches free from physical and pathological defects were randomly divided into two lots and stored at $0 \pm 0.5^{\circ}\text{C}$ and 95% relative humidity in two sealed neoprene containers of 1 m³ capacity. Ten plastic boxes containing about 3 kg of table grapes per box were stored in each container in the dark. One lot was stored under normal atmosphere for 33 days (non-treated fruit) and the other under a gas mixture containing 20% CO₂+20% O₂+60% N₂ (CO₂-treated fruit) for 3 days. The CO₂ concentration was maintained throughout the pretreatment experiment and was measured daily using an automated gas chromatograph system equipped with a thermal conductivity detector and Poraplot Q column (Varian Chrompack CP20033P). After 3 days, CO₂-treated grapes were transferred to air under the same conditions as non-treated fruits until the end of the storage period. Ten clusters were sampled periodically, and berries from five clusters (approx. 300 g each cluster) were peeled and the skin and pulp were frozen in liquid nitrogen, grounded to a fine powder and stored at -80°C until analysis.

Cloning of PAL, CHS and APX partial cDNAs

Total RNA was extracted from the skin of grapes according to the method of [Salzman et al. \(1999\)](#). Partial cDNA clones of PAL, CHS and APX were obtained by

RT-PCR. cDNA synthesis was performed with 10 µg of a mixture of total RNA from the skin of grapes stored in air and CO₂ for 12 and 33 days. The reaction was carried out in the presence of 500 ng of oligo-dT with 100 U of Reverse Transcriptase (Ecogen). PAL, CHS and APX gene DNA fragments were obtained by PCR amplification using the cDNA as template and the combination of the sense and the antisense primers. A 668 bp fragment of PAL was amplified by combining the degenerate sense primer 5'-CAATGGCTNGGCCNCAYATHGAA-3' and the degenerate antisense primer 5'-AARCGNATGTARCTACTGGGGACG-3'. A 634 bp fragment of CHS was amplified using a sense primer 5'-TGATTACTACTTCGCATCACCA-3' and the antisense primer 5'-CTTCCTTCTCTTTGACTCTCGTTGA-3'. A 539 bp fragment of APX was amplified using a degenerate sense primer 5'-GCATGGCACTCTGCTGGWAC-3' and the degenerate antisense primer 5'-TCATCSG-CAGCRTATTYTC-3'. PCR products were cloned into the pGEMT vector (Promega) and confirmed by sequencing.

RNA gel blot hybridization

Samples of denatured total RNA (10 µg) from the skin of grapes were fractionated and blotted as described in [Sanchez-Ballesta et al. \(2000\)](#). Equal loading was confirmed by ethidium bromide staining and by membrane staining with methylene blue. The DNA probe was random-primer labeled with $\alpha^{32}\text{P}$ -dCTP. Filters were prehybridized and hybridized at 65°C in 7% sodium dodecyl sulfate, 0.33 M phosphate buffer, pH 7.2, and 1 mM EDTA, then washed twice in $2 \times \text{SSC}$, 0.1% SDS at room temperature and twice in $0.1 \times \text{SSC}$, 0.1% SDS at 65°C and exposed to Kodak X-Omat SX film at -80°C . Methylene blue stained membranes and autoradiographs were digitally scanned and quantification was performed using a computer-assisted image analysis system (Scion Corporation, Frederick, MD). To ensure the accuracy of the changes in mRNA abundance and equal loading of RNA, the optical density values achieved in each Northern were normalized to the amount of 18S rRNA on the methylene blue staining. The 100% was assigned to the maximum optical density after normalization to the 18S rRNA in each Northern and the rest of optical densities were normalized to the maximum value and expressed as percentage of relative accumulation (RA).

PAL activity assay

PAL was extracted from 5 g of skin according to the method of [Faragher and Chalmers \(1977\)](#). The skin was ground in 25 ml of 100 mM H₃BO₃-NaOH buffer (pH 8.8) containing 25 mM 2-mercaptoethanol and 6% PVP. Afterwards, it was filtered through two layers of gauze and centrifuged for 30 min at 14,000g. The supernatant was saturated with 70% (NH₄)₂SO₄ and the pellet was sedimented by centrifuging 14,000g for 30 min, redissolved in the same buffer and used for the enzyme assay.

The assay was based on the method of [Tanaka et al. \(1974\)](#). The reagent mixture containing 2.5 ml of 100 mM borate-NaOH buffer (pH 8.8) and 0.5 ml of 40 mM

phenylalanine was preincubated at 30 °C for 5 min and the enzyme was added into the solution. The assay continued for 30 min at 30 °C and was stopped by adding 0.5 ml of 2 M perchloric acid. Prior to determination of OD at 280 nm, the mixture was centrifuged at 2000g for 15 min. The control tube included perchloric acid at the start of the assay. Specific enzyme activity was defined as nmol of cinnamic acid/h/mg of protein.

Protein concentration was measured by the method of Bradford (1976) using protein-dye reagent (Bio-Rad, Hercules, CA) and bovine serum albumin (Sigma-Aldrich, St Louis, MO) as a standard.

Analysis of total anthocyanin content

Total anthocyanin contents were determined by the pH differential method as reported by Wrolstad (1976). Briefly, skin samples (0.5 g) homogenized in liquid nitrogen were extracted with 0.01% HCl in 0.5 ml methanol using ultrasonication with cold water, four times for 10 min each. The extracts were centrifuged at 4000g and the supernatants were removed and filtered. Absorbance was measured in a UV-VIS spectrophotometer (UV-VIS 1601 Shimadzu) at 510 nm and at 700 nm in buffers at pH 1.0 and 4.5 using $A = ((A_{510} - A_{700}) \text{ pH}_{1.0} - [(A_{510} - A_{700}) \text{ pH}_{4.5}])$ with a molar extinction coefficient of malvidin-3-glucoside of 28,000 $\text{L mol}^{-1} \text{cm}^{-1}$. The results were expressed as milligrams of malvidin-3-glucoside equivalent per gram fresh weight (FW).

Radical cation ABTS scavenging capacity

The extraction of skin samples was performed in the same way as anthocyanin extraction described above. The radical cation 2,2'-azino-bis(3-ethylbenzothiazoline 6-sulphonate) (ABTS^+) scavenging capacity was measured as described by Rice-Evans et al. (1996), where ABTS^+ is oxidized with potassium persulfate. Trolox (Hoffman-La Roche; 6-hydroxy 2,5,7,8-tetramethylchroman-2-carboxylic acid; 2.5 mM) prepared in ethanol was used as an antioxidant standard and for the calculation of scavenging capacity of grape skin extracts as trolox equivalent. The scavenging activity of grape skins extracts was calculated as mM Trolox equivalent (TE)/g FW.

Statistical analyses

Experimental data are the mean \pm SE of three replicate samples of the determination for each sample. A variance analysis (one-way ANOVA) using the Fisher's least significant difference test (Statgraphics 5.1 Plus program, STSC, Rockville, MD) was performed to determine whether the total anthocyanin content, antioxidant activity and PAL activity induced in treated and non-treated grapes stored at 0 °C showed significant differences ($p \leq 0.05$).

Results

Total anthocyanin content and antioxidant activity in non-treated and CO_2 -treated grapes stored at 0 °C

Total anthocyanin content increased significantly after 12 days at 0 °C both in non-treated and CO_2 -treated grapes although it was higher in non-treated ones (Fig. 1). Thereafter, the accumulation of total anthocyanin decreased in both treated and non-treated fruit although at the end of the storage the accumulation was higher in non-treated grapes.

In CO_2 -treated grapes, antioxidant activity was higher than in non-treated fruit (Fig. 2). The antioxidant capacity in non-treated grapes decreased significantly along the storage reaching minimum by day 22 at 0 °C (Fig. 2). In CO_2 -treated fruit, changes in antioxidant capacity during storage at 0 °C were not significant, remaining similar to those achieved in freshly harvested grapes.

Effect of high CO_2 levels on anthocyanin gene expression (PAL, CHS) and PAL activity during low-temperature storage of grapes

To investigate the pattern of anthocyanin gene expression in response to a 3-day CO_2 pretreatment, total mRNA prepared from the skin of CO_2 -treated and non-treated grapes stored at 0 °C for up to 33 days was analyzed by northern hybridization, and PAL activity was determined.

The partial cDNA clones used as probes were obtained by RT-PCR (PAL, GenBank accession no.

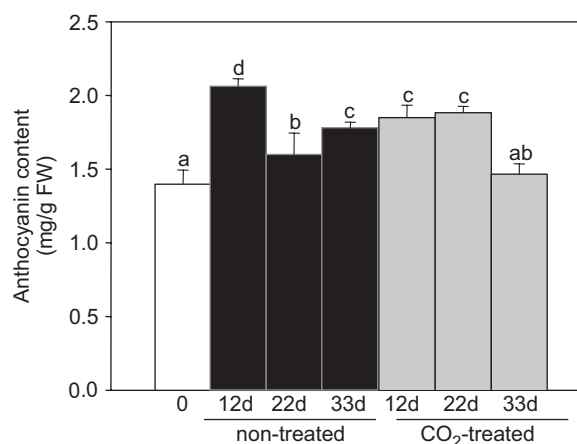


Fig. 1. Changes in total anthocyanin content in the skin of non-treated and CO_2 -treated 'Cardinal' table grapes stored at 0 °C. Results are the mean of three replicate samples \pm SE. Values labeled with the same letter are not different at the 5% significance level.

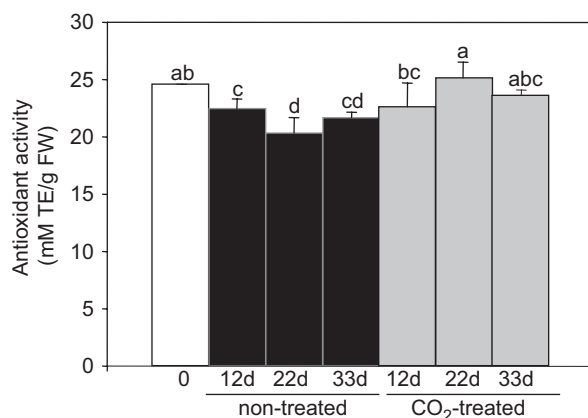


Fig. 2. Changes in antioxidant activity expressed as TE (mM/g FW) of non-treated and CO₂-treated 'Cardinal' table grapes stored at 0 °C. Results are the mean of three replicate samples \pm SE. Values labeled with the same letter are not different at the 5% significance level.

DQ887093 and CHS, GenBank accession no. DQ887094). The partial *VcPAL* cDNA consisted of 668 bp and encoded a polypeptide of 222 amino acids. The partial amino-acid sequence shared about 93% identity with PAL sequences from lemon, mandarin fruit and aspen. As regards *V. vinifera* PAL sequences, the deduced PAL amino-acid sequence showed 35% identity with a PAL sequence from the cultivar Cabernet Sauvignon (GenBank accession no. BAA31258) and 92% identity with a PAL from Lambrusco (GenBank accession no. X75967). The partial *VcCHS* cDNA consisted of 634 bp and encoded a polypeptide of 211 amino acids. A comparison of the partial deduced amino-acid sequence revealed that it was highly homologous (98% identity) to different CHS sequences from *V. vinifera* (Cv. Cabernet Sauvignon, CHS2 GenBank accession no. AB66275, psCH4 GenBank accession no. AB015872; Cv. Lambrusco Foglia Frastagliata, CHS GenBank accession no. X75969).

Storage of grapes at 0 °C induced the accumulation of *PAL* and *CHS* mRNA levels in the skin of non-treated and CO₂-treated grapes (Fig. 3A). However, both the *VcPAL* and the *VcCHS* mRNA levels in non-treated grapes were higher than in CO₂-treated fruit. In non-treated grapes, a sharp increase was observed in the levels of *PAL* mRNA after 12 days at 0 °C reaching the maximum by day 28 and decreasing thereafter. The accumulation of *CHS* transcript, on the other hand, was slow but progressive, reaching maximum after 28 days at 0 °C like the *PAL* mRNA and decreasing in the levels by day 33. In CO₂-treated grapes, the levels of *VcCHS* transcripts increased after 19 days and did not change until the end of the storage. Also, the *VcPAL* transcript levels

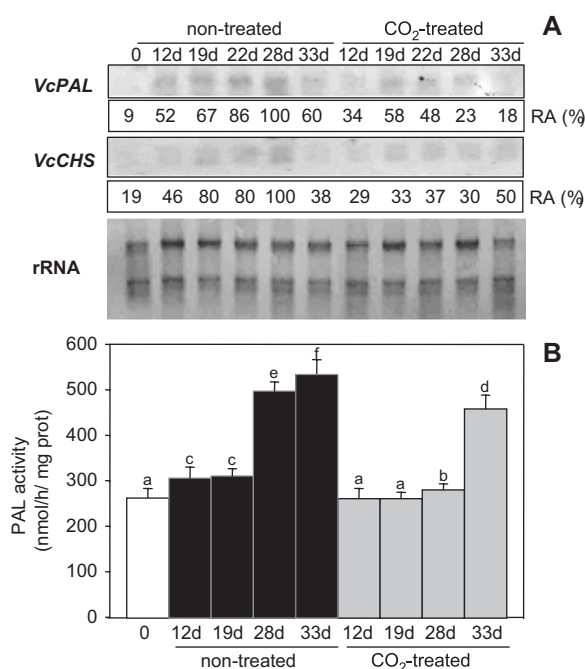


Fig. 3. Effect of high CO₂ pretreatment on *VcPAL* and *VcCHS* mRNA accumulation in the skin of 'Cardinal' table grapes stored at 0 °C (A). Ten micrograms of total RNA from the skin was fractionated by gel electrophoresis, blotted and hybridized with the partial *VcPAL* and *VcCHS* probes. The equivalence of RNA loading of the lanes was demonstrated by methylene blue staining. The intensity of the bands was quantified by scanning densitometry of the autoradiographs and it was normalized to the amount of 18S rRNA on the methylene blue staining. Optical density values were normalized to the maximum value and expressed as percentage of RA. (B) Time courses of PAL activity in the skin of non-treated and CO₂-treated 'Cardinal' table grapes stored at 0 °C. Data are the average of two separate experiments ($n = 6$) \pm SE. Values labeled with the same letter are not different at the 5% significance level.

increased after 19 days and decreased after 33 days. Transcript levels remained lower than that in non-treated grapes throughout storage. As probes were used the partial cDNAs isolated showed high homology with different *PAL* and *CHS* sequences, indicating that global expression of different isogenes could be measured. Northern analysis revealed that *PAL* and *CHS* gene expression was not detected in the pulp of either treated or non-treated grapes (data not shown).

PAL activity increased slightly in non-treated grapes after 12 days at 0 °C, showing a sharp increase by day 28, paralleled to the higher accumulation in *PAL* transcript and reaching maximum after 33 days (Fig. 3B). PAL activity was significantly lower in CO₂-treated grapes than that

in non-treated fruit reaching maximum by day 33, although this maximum was lower than that recorded in non-treated grapes, the same pattern as in PAL mRNA accumulation.

Effect of high CO₂ levels on APX gene expression during low-temperature storage of grapes

A partial APX cDNA clone was obtained by RT-PCR using as template a mixture of cDNAs synthesized from total RNA extracted from the skin of CO₂-treated and non-treated grapes stored at 0 °C. A cDNA fragment of 539bp was cloned and named VcAPX (GenBank accession no. [DQ887095](#)). The deduced sequence of 179 amino acid presented the heme-binding domain that share all APX proteins, and it showed 82–98% similarity with amino-acid sequences of APX genes accessed in GenBank, being the greatest similarity to cytosolic APX sequences.

VcAPX transcript levels increased in non-treated grapes after 12 days, reaching maximum by day 28 and decreasing thereafter (Fig. 4). In CO₂-treated grapes, on the other hand, the increase in the accumulation of the transcript was smaller and did not change during storage at 0 °C.

Discussion

The use of high CO₂ concentrations to enhance table grapes quality in place of SO₂ fumigation has been a focus of interest in recent years (Crisosto et al., 2002; Retamales et al., 2003; Artés-Hernández et al., 2006; Romero et al., 2006; Sanchez-Ballesta et al., 2006). However, there is little understanding of its possible mode of action, although many authors have reported that high CO₂ treatments maintain grape quality by retarding fungal attack, mainly caused by *B. cinerea*. In previous works, we observed that a 3-day high CO₂ pretreatment significantly reduced natural fungal decay in table grapes cv. Cardinal stored at 0 °C for up to 33 days, but that this beneficial effect was not mediated by the induction of PRs and STS gene expression (Romero et al., 2006; Sanchez-Ballesta et al., 2006). STS and CHS, the enzymes of resveratrol and anthocyanin biosynthesis respectively, each catalyze the formation of a tetraketide intermediate from a CoA-tethered phenylpropanoid starter and three molecules of malonyl-CoA, but use different cyclization mechanisms to produce the end products. Likewise, PAL catalyzes the first step of the multi-branched general phenylpro-

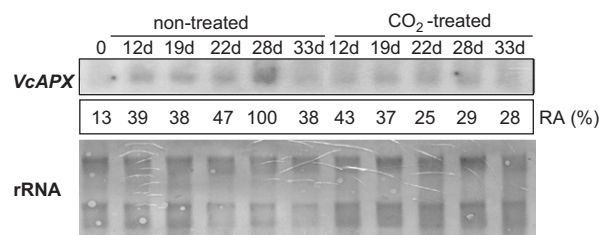


Fig. 4. Effect of high CO₂ pretreatment on VcAPX mRNA accumulation in the skin of 'Cardinal' table grapes stored at 0 °C. Ten micrograms of total RNA from the skin was fractionated by gel electrophoresis, blotted and hybridized with the partial VcAPX probe. The equivalence of RNA loading of the lanes was demonstrated by methylene blue staining. The intensity of the bands was quantified by scanning densitometry of the autoradiographs, and it was normalized to the amount of 18S rRNA on the methylene blue staining. Optical density values were normalized to the maximum value and expressed as percentage of RA.

panoid pathway, which supplies substrates for biosynthesis of different phenolic compounds such as the end products of the reactions catalyzed by the STS and CHS enzymes. Since we observed that high CO₂ pretreatment did not modulate STS gene expression to control fungal decay, a new area of research is open to further investigate the molecular mechanisms implicated in the mode of action of high CO₂ concentrations in table grapes by analyzing anthocyanin biosynthesis gene expression.

The total anthocyanin content increased in both treated and non-treated grapes after 12 days of storage at 0 °C, decreasing thereafter, reaching in CO₂-treated grapes levels similar to those observed in freshly harvested grapes (Fig. 1) after 33 days. This trend in anthocyanin levels match with a decrease in *L*^{*}, Croma and hue angle color parameters, although no significant changes between treated and non-treated grapes were quantified (data not shown). Mori et al. (2005) demonstrated that environmental factors affect anthocyanin synthesis in grape berries through the regulation of PAL activity and CHS gene expression. They showed that anthocyanin synthesis, PAL activity and CHS3 transcript levels in Darkridge grapes were markedly higher in berries grown under low night temperatures. It is already known that anthocyanin synthesis continues after harvesting and also in low-temperature storage (Kalt et al., 1999). The application of high CO₂ as a pretreatment in table grapes causes an increase in the total anthocyanin content during storage at 0 °C, although this increase was lower than that in non-treated grapes.

By contrast, it has been reported that CA or MAP treatments inhibit postharvest increase of anthocyanin concentrations in different fruits (Gil et al., 1997; Remon et al., 2004). Nevertheless, Veazie and Collins (2002) reported that total monomeric anthocyanin in Navaho blackberries held in CA storage at 2 °C increased in the first 3 days and decreased thereafter.

The increase of total anthocyanin content in treated and non-treated grapes did not produce any increase in antioxidant activity during low-temperature storage (Fig. 2). However, it is interesting to note that although antioxidant activity in the treated grapes stored at low temperature was similar to that of freshly harvested fruit, it decreased in the non-treated fruit. No changes in antioxidant activity were detected in apples stored at low temperatures and under CA conditions (van der Sluis et al., 2001), but there was a decrease in antioxidant activity of samples of fresh-cut spinach stored under MAP at 10 °C (Gil et al., 1999).

To analyze anthocyanin biosynthesis gene expression, we have isolated partial cDNAs encoding PAL and CHS from the skin of table grapes. The predicted VcPAL amino-acid sequence shared significant levels of identity with the published sequence from *V. vinifera* Cv. Lambrusco (Sparvoli et al., 1994) as well as from other plant species. The present work shows that the high CO₂ pretreatment that significantly reduced natural fungal decay in table grapes stored at 0 °C prevented the large increase in VcPAL transcript levels observed in non-treated grapes (Fig. 3A). The PAL gene expression is also elicited in this way in grapevine leaves infected with *B. cinerea* (Bezier et al., 2002). Furthermore, the increase in PAL activity was higher in non-treated grapes (Fig. 3B). PAL was one of the first plant “defense genes” identified, and both PAL mRNA levels and PAL activity could be induced by a wide array of environmental cues, such as pathogen attack, low temperatures, UV irradiation, mechanical wounding, and light (Lawton and Lamb, 1987; Gläbgen et al., 1998; Kamo et al., 2000; Sanchez-Ballesta et al., 2000). PAL expression and activity may therefore be considered a good marker to investigate the process whereby high CO₂ levels effectively control the grape decay. The PAL activation observed in untreated cherimoya fruit after prolonged storage at chilling temperature was reduced by an effective high CO₂ pretreatment (Maldonado et al., 2002). Likewise, in mandarin fruit an effective heat treatment prevented the increase in PAL activity that normally occurs around the necrotic zones of fruits when stored at low

temperatures (Martínez-Téllez and Lafuente, 1997; Sanchez-Ballesta et al., 2000). The results of the present work, then, reinforce the idea that PAL may be implicated in defense responses against natural fungal infection in non-treated grapes but not in the mechanisms operating in treated grapes to reduce total decay.

In grapevine, the copy number of CHS has been estimated at three to four. The predicted partial VcCHS amino-acid sequence shared more than 90% identity with the three different grapevine CHS deposited in the databases, showing the closest homology to CHS2 (Goto-Yamamoto et al., 2002). The 3-day CO₂ pretreatment also reduced the increase in the VcCHS transcript levels observed in non-treated grapes (Fig. 3A). When it was compared with VcPAL gene expression in non-treated grapes stored at 0 °C, the increase in VcCHS mRNA was later and progressive, but the maximum in both PAL and CHS gene expression was observed by day 28. The activities of CHS are largely regulated at the transcription level. The expression of CHS genes is controlled by developmental stages of the plant, as well as by biological and environmental stresses such as low temperature, pathogen attack and wounding (Junghans et al., 1993; Leyva et al., 1995; Seki et al., 1999). Table grapes stored at low temperatures in air respond to natural fungal decay with a large increase in PAL and CHS gene expression, PAL activity and total anthocyanin content. In this respect, the lower VcPAL and VcCHS mRNA levels in CO₂-treated fruit might constitute cellular signals indicating a lower rate of stress imposition. Furthermore, this protective effect of high CO₂ pretreatment is concomitant with a decrease in the induction of APX gene expression. We have also isolated a partial cDNA encoding a cytosolic APX. At present, there are many reports about cytosolic APX in different plants and fruits (Mittler and Zilinskas, 1991; Ishikawa et al., 1995; Kim and Chung, 1998), but there are no reports on table grapes related to APX gene. In the present study, the analysis of APX gene expression revealed that transcript levels increased slightly both in treated and non-treated grapes, but a sharp increase was observed after 28 days in non-treated grapes where total decay was evident (Romero et al., 2006). These results indicate differences in the mechanisms operating in treated and non-treated grapes, suggesting that APX participate in removing the putative high levels of H₂O₂ in non-treated grapes. APX seems to be activated during compatible interactions (Garcia-Limones et al., 2002), and many reports indicated that it is even inhibited during resistance or during pathogen-induced programmed cell death (Mittler et al., 1998).

The evidences provided here suggest that the effectiveness of high CO₂ pretreatment to control fungal decay maintaining fruit quality after prolonged low-temperature storage is the result of ability to prevent the formation of ROS rather than their inactivation once formed. Further analysis is needed to ascertain the role of anthocyanin induced during low-temperature storage and to identify responses associated with the antioxidant systems that participate in the beneficial effect of CO₂ treatment.

Acknowledgements

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ARTÍCULO 4

Individual anthocyanins and their contribution to total antioxidant capacity in response to low temperature storage and high CO₂ in Cardinal table grapes.

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***Postharvest Biology and Technology* (aceptado)**

RESUMEN

En este estudio, hemos analizado los perfiles de los antocianos individuales en la piel de la uva de mesa y su contribución a la capacidad antioxidante total (TAC) en respuesta a bajas temperaturas (0°C) y altos niveles de CO₂ (20 % durante 3 días). También se determinó el análisis de los parámetros representativos de color de esta variedad roja-violeta. La composición de antocianos fue determinada usando HPLC-DAD-MS. La contribución de los antocianos individuales al valor TAC de uvas de mesa fue calculado basándonos en su concentración y capacidad antioxidante medido como valor TEAC (pendiente de antocianos/pendiente Trolox). Los análisis cromatográficos identificaron seis antocianos en la piel de uvas de mesa Cardinal, incluyendo pelargonidina-3-glucósido (Pg-3-G). Tiempos cortos de almacenamiento a 0°C en aire tuvieron como efecto incrementar la concentración de cada antociano identificado. Después de 3 días a 0°C, las uvas no tratadas presentaron el mayor contenido en antocianos (27.55 mg/100gFW) y presentaron el mayor valor TAC (52.45 mM/100gFW). La peonidina-3-glucósido (Pn-3-G), antociano predominante en esta variedad de uva roja, fue la principal responsable del aumento de los valores TAC en uvas de mesa no tratadas. La Pn-3-G tuvo un bajo valor de TEAC (1.73 mM), pero su contribución podría ser explicada por el gran aumento encontrado en el contenido de este antociano los primeros días de almacenamiento a 0°C. Por el contrario, al final del tratamiento con CO₂, el contenido de Pn-3-G no cambió, y tanto el contenido de antocianos como el valor TAC de uvas de mesa tratadas con CO₂ fueron similares a los encontrados en uvas antes de la conservación. Además, el tratamiento con CO₂ llevó a un aumento significativo en el contenido de Pg-3-G, concomitante con una bajada pronunciada en delfinidina-3-glucósido (Dp-3-G) y menores

descensos en petunidina-3-glucósido (Pt-3-G) y malvidina 3-glucósido (Mv-3-G). Estos efectos de los altos niveles de CO₂ en el perfil de antocianos individuales se fueron perdiendo progresivamente cuando las uvas fueron transferidas a aire. De hecho, después del almacenamiento prolongado a bajas temperaturas, se cuantificaron valores de TAC similares en uvas no tratadas y aquellas expuestas al pretratamiento con 20% de CO₂. Estos datos abren nuevas perspectivas sobre el efecto de bajas temperaturas y altos niveles de CO₂ en la concentración de antocianos individuales identificados en uvas de mesa Cardinal.



Individual anthocyanins and their contribution to total antioxidant capacity in response to low-temperature storage and high CO₂ in cardinal table grapes

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Abstract

In this study, we have analyzed the profiles of individual anthocyanins in the skin of cardinal table grapes and their contribution to the total antioxidant capacity (TAC) in response to low temperature (0 °C) and high CO₂ levels (20% for 3 days). An analysis of the representative colour parameters of this red-violet variety was also determined. The anthocyanin composition was determined using high-performance liquid chromatography coupled to diode array detector and mass spectrometry (HPLC–DAD–MS). The contribution of individual anthocyanins to the TAC value of table grapes was calculated on the basis of their concentration and antioxidant capacity measured as the TEAC value (slope of the anthocyanin/slope of Trolox). Chromatographic analysis identified six anthocyanins, including pelargonidin 3-glucoside (Pg-3-G), in the skin of cardinal table grapes. Short-term storage at 0 °C in air had an increasing effect on the concentration of each of the identified anthocyanins. After 3 days at 0 °C, untreated grapes had the highest anthocyanin content (27.55 mg/100 g FW) and displayed the largest TAC value (52.45 mM TE/199 g FW). Peonidin 3-glucoside (Pn-3-G) was the predominant anthocyanin, and it was mainly responsible for the rise in the calculated TAC value in untreated grapes. Pn-3-G had a low average TEAC value (1.73 mM), but its contribution could be explained by the sharp increase in the content of this anthocyanin the first days of storage at 0 °C. In contrast, the Pn-3-G content in grapes at the end of the 3-day CO₂ treatment did not change, and both the total anthocyanin content and the calculated TAC value remained significantly constant in comparison to the levels in pre-stored grapes. In addition CO₂ treatment had a positive effect on the amount of Pg-3-G concomitant with a pronounced decline in delphinidin 3-glucoside (Dp-3-G) and smaller decreases in petunidin 3-glucoside (Pt-3-G) and malvidin 3-glucoside (Mv-3-G). These effects of high CO₂ levels on the profile of individual anthocyanins were progressive lost when grapes were transferred to air. Indeed, after prolonged low-temperature storage when the colour of the berries become dark violet, similar calculated TAC values were quantified in untreated grapes and in those exposed to 20% CO₂. These data provide new insights about the effect of low temperature and high CO₂ levels on the concentration of the individual anthocyanins identified in cardinal table grapes.

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Keywords: Table grapes; Post-harvest technology; Carbon dioxide; Low temperature; Anthocyanins profile; Total antioxidant capacity

1. Introduction

Low temperature is one of the most effective technologies to extend the post-harvest storage life of table grapes. Although *Vitis vinifera* is tolerant to chilling, activation of the defense in responses to stress have been reported in cardinal table grapes. Specifically, we observed a transitory increase in the abundance of *PAL* and *CHS* transcripts during the first 3

days of storage at 0 °C in the skin of untreated grapes, which was accompanied by an increase in total anthocyanin content (Sanchez-Ballesta et al., 2007). Indeed, cold temperature has been seen to increase anthocyanin levels in several growing plant species (Christie et al., 1994; Faragher, 1983; Oren-Shamir and Levi-Nissim, 1997; Shichijo et al., 1993; Stiles et al., 2007). Although this phenomenon appears to be relatively common, there is still some uncertainty concerning the significance of increased anthocyanin production during post-harvest storage at low temperature. Indeed, the effect of low temperature on the concentration and distribution of anthocyanin pigments, and on their antioxidant activity, has yet to be fully characterized.

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Anthocyanins are usually present in plants as a mixture of major and minor compounds. Their separation and identification requires the use of reversed-phase high-performance liquid chromatography (HPLC) with diode array detection (DAD), which is effective in analyzing these pigments (Hong and Wrolstad, 1990). However, the natural variability of different anthocyanins is large and some of them present similar retention times and spectral characteristics, making their identification by HPLC–DAD alone difficult. Therefore other techniques are often needed to accurately identify and characterize minor pigments. Among these techniques, mass spectrometry and MSⁿ analysis, coupled to the HPLC–DAD, are widely used to identify anthocyanins in different biological tissues (De Pascual-Teresa et al., 2002).

Several assays have been introduced to measure total antioxidant activity in food extracts and as such, it is often difficult to compare the results obtained for the same product in different studies. Furthermore, since antioxidant activity is derived from the delicate balance between antioxidants and prooxidants components, the total antioxidant capacity (TAC) of biological tissues in response to environmental conditions is sometimes not uniform. Hence, to calculate the TAC of table grapes during post-harvest storage we have considered the sum of the antioxidant capacity of the individual anthocyanins determined in the sample. The antioxidant activity of many anthocyanins was previously reported in terms of their Trolox equivalent antioxidant capacity (TEAC) (Awika et al., 2004; Solomon et al., 2006). However, differences in the protocols and calculation methods (De Beer et al., 2006) produce different TEAC values for the respective anthocyanins. Furthermore, while these values are useful to determine the relative importance of the respective phenolic compounds, published data cannot be used to calculate the contribution of individual compounds to the TAC of a given sample. Hence, the TEAC values of pure anthocyanin reference standards have been measured in this work using the same protocol as that employed to determine the TAC of table grapes stored under different environmental conditions.

Anthocyanins are also responsible for many red, violet and blue colours in fruits and flowers (Harbone and Grayer, 1988; Remon et al., 2004). Pelargonidins are primarily responsible for the orange, salmon, pink and red colour of the fruit, while the magenta and crimson comes from the cyanidins, and the purple, mauve, and blue are due to the delphinidins present. Since colour is an important parameter in berry quality, the association between colour and anthocyanin pigments profiles has been evaluated during post-harvest storage of table grapes. In this work, we applied the CIELAB colorimetric system to assess the changes in skin colour of untreated and CO₂-treated grapes during low-temperature storage.

The aim of the present work was to analyze the individual anthocyanins in red-violet table grapes and to define their changes in response to low-temperature storage (0 °C) after harvest. We also assessed how table grapes respond to high CO₂ levels (3 days, 20%) at 0 °C, both at the end of the treatment and when grapes were transferred to air. To associate anthocyanin production with important metabolic aspects of the fruit, we analyzed the contribution of individual anthocyanins to the TAC, as

well as their implication in the colour of the skin of the grapes when exposed to CO₂ or not. This information is essential to evaluate the efficiency of post-harvest technologies whose goals should be to maintain the health and quality of the intact fruit.

2. Materials and methods

2.1. Plant material

Early-harvesting mature table grapes (*V. vinifera* L. cv. Cardinal) from Sevilla (Spain) were used (12.7% total soluble solids, 0.81% tartaric acid). Forced-air pre-cooled bunches free from physical and pathological defects were randomly divided into two lots and stored at 0 ± 0.5 °C and 95% relative humidity (RH) in two sealed neoprene containers of 1 m³ capacity. Ten plastic boxes containing about 3 kg of table grapes per box were stored in each container. One lot was stored in air for 33 days (untreated fruit) and the other under a gas mixture of 20% CO₂ + 20% O₂ + 60% N₂ (CO₂-treated fruit) for 3 days. The CO₂ concentration was maintained throughout the pretreatment and was measured daily using an automated gas chromatography system equipped with a thermal conductivity detector and a Poraplot Q column (Varian Chrompack CP20033P). After 3 days, the CO₂-treated grapes were transferred to air under the same conditions as the untreated fruit until the end of the storage period. Ten clusters were sampled periodically. The berries from five clusters (approximately 300 g each cluster) were peeled and the skin was mixed, frozen in liquid nitrogen, ground to a fine powder and stored at –80 °C for further analysis. For colour analysis, 45 berries were used that were randomly removed from the other five clusters and distributed into three replicates of 15 berries each.

2.2. Extraction of anthocyanins

Frozen skin samples (0.5 g) were homogenized with 0.5 mL methanol containing 0.01% HCl by ultra-sonication for 10 min. The extract was centrifuged at 4000 × g and the supernatant was removed. This step was repeated twice with the same solvent system until no more pigment was extracted and the solvent remained clear. The combined supernatants were filtered through a 0.45 µm nylon membrane filter (Millipore), to remove the solids residues, and the filtered material was evaporated to dryness with N₂ gas before resuspending in an equal volume of acidified water containing 4.5% formic acid (v/v) and acetonitrile (95:5, v/v) for later HPLC–DAD–MS analysis.

2.3. HPLC–DAD–MS analyses

Aliquots of extracted anthocyanins (50 µL) were analyzed using a liquid chromatography/mass selective detector (LC/MSD) system coupled in series to a photodiode array detector (DAD, G1315B) consisting of a quaternary pump (G1311A), a vacuum degasser, a well-plate autosampler (G1313A) and a thermostat controlled column compartment controlled by software LC/MS ChemStation Revision A.08.03 from Agilent Technologies 1100 series (Waldbronn, Germany). Samples

were injected at room temperature (20 °C) and the components were separated using a reverse-phase C₁₈ column (150 mm × 4.6 mm, 5 µm particle size, Scharlab, Barcelona, Spain). The mobile phase consisted of acidified water containing 4.5% formic acid (v/v, A) and acetonitrile (B). The gradient used commenced with 5% phase B at time 0, 5–8% at 5–10 min, 8–10% at 10–15 min, 10–15% at 15–22 min, 15–25% at 22–27 min, 25–40% at 27–30 min, 40–73% at 30–33 min, 73–95% at 33–34 min, 95–5% at 34–41 min. The flow rate was 0.9 mL/min, and the wavelength of detection was set at 520 nm. Scanning was also performed from 450 to 800 nm in 2 nm steps. Electrospray mass spectrometric analyses were carried out in a positive ion mode using a quadrupole mass spectrometer (G1946D) fitted with an atmospheric pressure electrospray ionization source (API-ES) with a fragmentation voltage of 140 V. The conditions of the spray chamber were nebulizer, 45 psig; dry gas (N₂), 12 L/min; gas temperature, 300 °C; capillary voltage (positive), 3000 V. Spectra were recorded between *m/z* 287 and 494. The anthocyanin peaks were identified by comparison with molecular and main fragment ion values previously described in the literature (Muñoz-Espada et al., 2004; De Beer et al., 2006) and confirmed by comparison of commercially available anthocyanins standards. The anthocyanin concentrations were determined by the peak areas of the respective ion chromatograms extracted for delphinidin 3-*O*-glucoside (Dp-3-G), cyanidin 3-*O*-glucoside (Cy-3-G), petunidin 3-*O*-glucoside (Pt-3-G), pelargonidin 3-*O*-glucoside (Pg-3-G), peonidin 3-*O*-glucoside (Pn-3-G) and malvidin 3-*O*-glucoside (Mv-3-G), and using a standard curve derived from the commercial anthocyanins (Extrasynthese, France). The range of the calibration curves, with at least five points for each standard anthocyanin, took into account the relative abundance of table grape anthocyanins: 0–2 µg/mL for Pg-3-G, 1–10 µg/mL for Cy-3-G, 2–20 µg/mL for Dp-3-G and Mv-3-G and 2–300 µg/mL for Pn-3-G. The quantification for Pt-3-G was carried out in Pg-3-G equivalents and individual anthocyanin levels were expressed as mg/100 g fresh weight (FW).

2.4. Colour

Berry skin colour was measured at three different positions around the equator of the grape using the Hunter Lab System and a Minolta CR200TM colorimeter (Minolta Camera Co., Osaka, Japan). Results were given in Commission Internationale de l'Eclairage *L*^{*} (lightness), *a*^{*}, and *b*^{*} (CIELAB) colour space coordinates. The chroma ($a^2 + b^2$)^{1/2} and hue angle ($\tan^{-1} b/a$) were calculated.

2.5. Radical cation ABTS scavenging capacity

Trolox (6-hydroxy 2,5,7,8-tetramethylchroman-2-carboxylic acid, Hoffman-La Roche) and standard anthocyanins, Dp-3-G, Cy-3-G, Pn-3-G, Pg-3-G and Mv-3-G (Extrasynthese, France) were diluted with ethanol at different concentrations to evaluate their antioxidant capacity, in a linear range, by the radical cation 2,2'-azinobis(3-ethylbenzothiazolone 6-sulphonate) (ABTS^{•+}) as described by Re et al. (1999). The ABTS^{•+} solution was

diluted with ethanol to an absorbance of 0–70 (±0.02) at 734 nm and equilibrated at 30 °C. After adding 990 µL of diluted ABTS^{•+} solution to 10 µL aliquots of different concentrations of Trolox and standard anthocyanins (µM), the absorbance reading was taken at 30 °C exactly 1 min after the initial mixing, and then for up to 6 min. Appropriate solvent blanks were run in each assay. The inhibition of absorbance at 734 nm is calculated and plotted as a function of the antioxidant concentration, and of the inhibition produced by Trolox as the standard reference compound.

The TAC contribution (mM TE/100 g FW) of individual anthocyanins in the skin of table grape was calculated from their anthocyanins content (mg/100 g FW) and TEAC values (mM) as described by De Beer et al. (2006):

- TEAC = slope (test compound)/slope (Trolox).
- TAC contribution = [compound] × TEAC.

2.6. Statistical analyses

Data from at least three replicates per sampling period were subjected to an analysis of variance (ANOVA, Statgraphics program, STSC, Rockville, MD), and a multiple variance analysis was used to determine the significance of the data at $P \leq 0.05$. Two-way analysis of variance was performed using the LSD test procedure with type III sums of squares and a confidence level of 95% (Statgraphics program, STSC, Rockville, MD). The main effects of high CO₂ treatment, time of storage at 0 °C, and the CO₂ treatment × time interaction on fruit were assessed.

3. Results

3.1. Identification of anthocyanins

By combining HPLC–DAD and the analysis of the MS spectra, six anthocyanins were identified in Cardinal table grapes (Fig. 1), whose retention times, molecular ions and main fragment ions are summarized in Table 1. Of these, peak 5 was associated with a strong signal in the MS detector and it corresponded to Pn-3-G. The MS spectrum revealed a molecular ion at *m/z* 433.3 associated with peak 4 and the main ion fragment produced was 271, corresponding to Pg-3-G. Additionally, a comparison of the molecular ions and ion products of these anthocyanins with those of commercially available anthocyanin

Table 1
Chromatographic and spectrophotometric characteristics of each identified anthocyanins in cardinal table grape

Peak number	Retention time (min)	Molecular ion (<i>m/z</i>)	Main fragment ions	Peak assignment
1	4.78 ± 0.16	465.3	303	Dp-3-G
2	7.14 ± 0.32	449.2	287	Cy-3-G
3	8.95 ± 0.39	479.4	317	Pt-3-G
4	10.35 ± 0.40	433.3	271	Pg-3-G
5	12.12 ± 0.39	463.3	301	Pn-3-G
6	14.17 ± 0.35	493.4	331	Mv-3-G

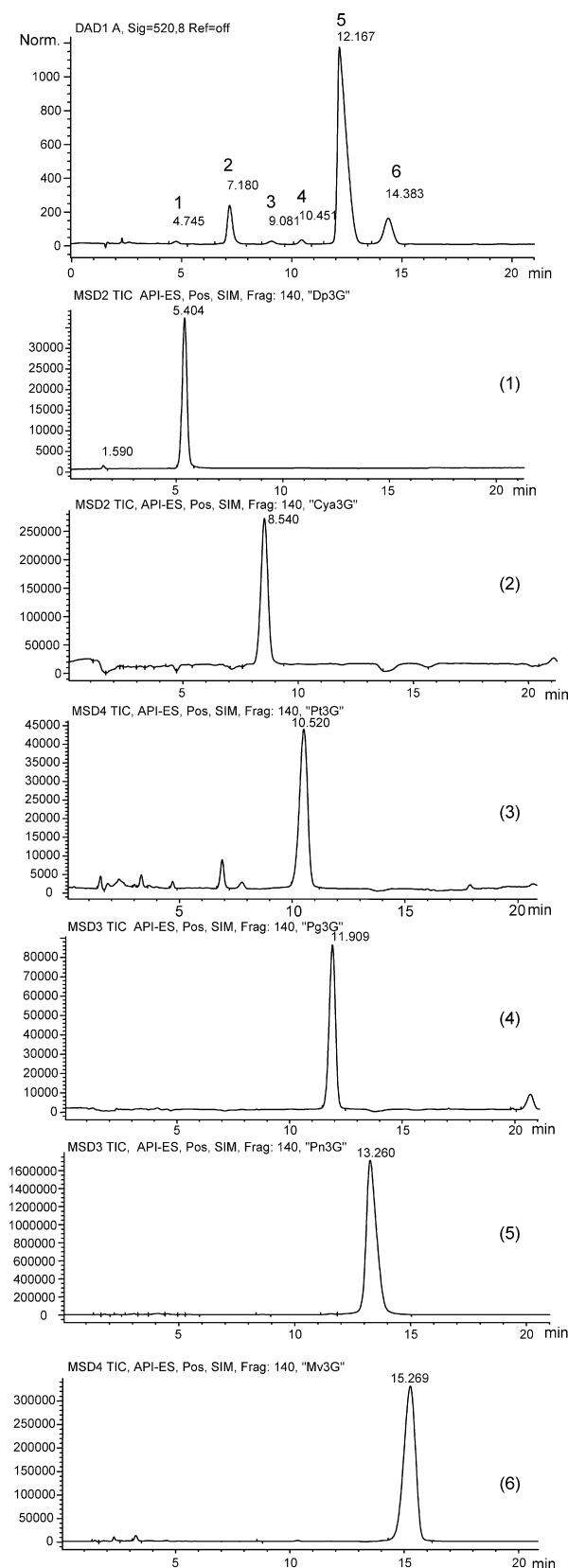


Fig. 1. HPLC-DAD chromatogram (520 nm) and the ion chromatograms extracted at m/z corresponding to the molecular ion of each identified anthocyanins in cardinal table grape: (1) delphinidin-3-glucoside; (2) cyanidin-3-glucoside; (3) petunidin-3-glucoside; (4) pelargonidin-3-glucoside; (5) peonidin-3-glucoside; (6) malvidin-3-glucoside.

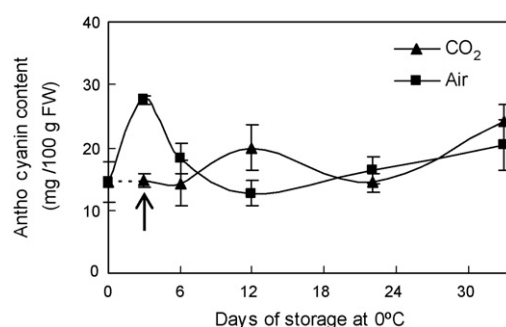


Fig. 2. Changes in anthocyanin content as result of the sum of the individual anthocyanins identified and quantified in untreated and CO₂-treated cardinal table grapes during storage at 0°C. The dotted line indicates the short period of high CO₂ treatment. The row indicates the transfer of CO₂-treated fruit to air. The results are the mean of three replicate samples \pm S.E.

standards confirmed the identification of Dp-3-G, Cy-3-G, Pn-3-G, Pg-3-G, Mv-3-G and Pt-3-G.

3.2. Content and distribution of individual anthocyanins in table grapes in response to low temperature and short-term exposure to high levels of CO₂

The change in the anthocyanin content as result of the sum of the six individual anthocyanins during storage at 0°C was examined (Fig. 2), and the anthocyanin levels in CO₂ treated grapes were quantified at the end of the treatment and when grapes were transferred to air. While 3 days of storage in air induced a sharp increase in the anthocyanin content from 14.55 to 27.55 mg/100 g FW, exposure to high levels of CO₂ did not cause any change with respect to the values of pre-stored grapes. After 6 days storage at 0°C, the elevated anthocyanin content observed in untreated grapes decreased, reaching values similar to those found in CO₂-treated ones. In contrast, the anthocyanin content of CO₂-treated grapes transferred to air increased after 12 days and was still higher than that in untreated grapes at the end of the storage period.

The individual concentration of anthocyanins found in table grapes at the end of the CO₂ treatment and in those stored in air was determined at the same chronological age (3 days) (Table 2). Pn-3-G was the predominant anthocyanin found in this variety, with values of 12.78 mg/100 g FW in pre-stored table grapes. In untreated fruit stored in air for 3 days, there was an important increase in Pn-3-G content (+97%), reaching values of 25.20 mg/100 g FW. There was also a sharp increase in the minor anthocyanin Pg-3-G (+141%), from 0.061 to 0.147 mg/100 g FW. The first days of storage at 0°C had a less pronounced effect on Cy-3-G (+49%), Dp-3-G (+48%) and Pt-3-G (+25%), and only a moderate effect on the Mv-3-G content (+18%). While exposure for 3 days to high CO₂ treatment did not effect the Pn-3-G content (0%) and it had only a moderate effect on the Cy-3-G content (+24%), it sharply increased the Pg-3-G (+200%). In contrast to the increase observed in grapes stored in air, high CO₂ treatment caused a pronounced decrease in Dp-3-G (−64%) and smaller decreases in Mv-3-G (−21%) and Pt-3-G (−27%) with respect to the content in pre-stored grapes.

Table 2

Individual anthocyanin content (mg/100 g FW) in untreated and CO₂-treated grapes after 3 days at 0 °C

	Days at 0 °C				
	0 day	3-day air	Δ (%) ^a	3-day CO ₂	Δ (%) ^b
Pn-3-G	12.78 ± 3.09 a ^c	25.20 ± 0.33 b	+97	13.08 ± 0.84 a	0
Cy-3-G	0.41 ± 0.01 a	0.61 ± 0.12 b	+49	0.51 ± 0.06 a,b	+24
Pg-3-G	0.061 ± 0.003 a	0.147 ± 0.007 b	+141	0.183 ± 0.009 c	+200
Mv-3-G	1.14 ± 0.10 a,b	1.35 ± 0.14 b	+18	0.90 ± 0.18 a	−21
Dp-3-G	0.123 ± 0.015 b	0.182 ± 0.004 c	+48	0.044 ± 0.015 a	−64
Pt-3-G	0.048 ± 0.002 b	0.060 ± 0.005 c	+25	0.035 ± 0.002 a	−27

^a Delta between those two time points $t=0$ and $t=3$ -day air.^b Delta between those two time points $t=0$ and $t=3$ -day CO₂.^c Different letter in a row indicate a significant difference ($P \leq 0.05$).

The change in the proportion of individual anthocyanins relative to the total anthocyanin content was determined in untreated grapes during storage at 0 °C and in CO₂ treated grapes at the end of the treatment and when the grapes were transferred to air (Fig. 3). Pn-3-G was the main anthocyanin, accounting for 87.8% of anthocyanin content in pre-stored grapes. After 3 days storage at 0 °C, a rise in the percentage of Pn-3-G was observed in untreated grapes. By contrast, Pn-3-G content was similar to the values found in pre-stored grapes after the CO₂-treatment. Interestingly, at the end of the 3-day CO₂ treatment there was a pronounced decrease in the anthocyanins synthesized directly from dihydromyricetin in the grapes, namely Dp-3-G, Mv-3-G and Pt-3-G, concomitant with

a marked increase in the 3-*O*-glucoside of pelargonidin. After 6 days storage at 0 °C, the sharp rise both in the anthocyanin content and in the percentage of Pn-3-G observed in the first days of storage in untreated grapes decreased, reaching levels similar to those observed in the CO₂-treated fruit. Thus, our results showed that when CO₂-treated grapes were transferred to air, the percentage of Cy-3-G and Pg-3-G dropped sharply while the proportion of Mv-3-G, Dp-3-G and Pt-3-G began to increase, reaching similar values to those detected in untreated grapes after 12 days in storage. Thereafter, the trend in the percentage of individual anthocyanins was virtually identical in untreated grapes and those exposed to CO₂, finally reaching the same proportions.

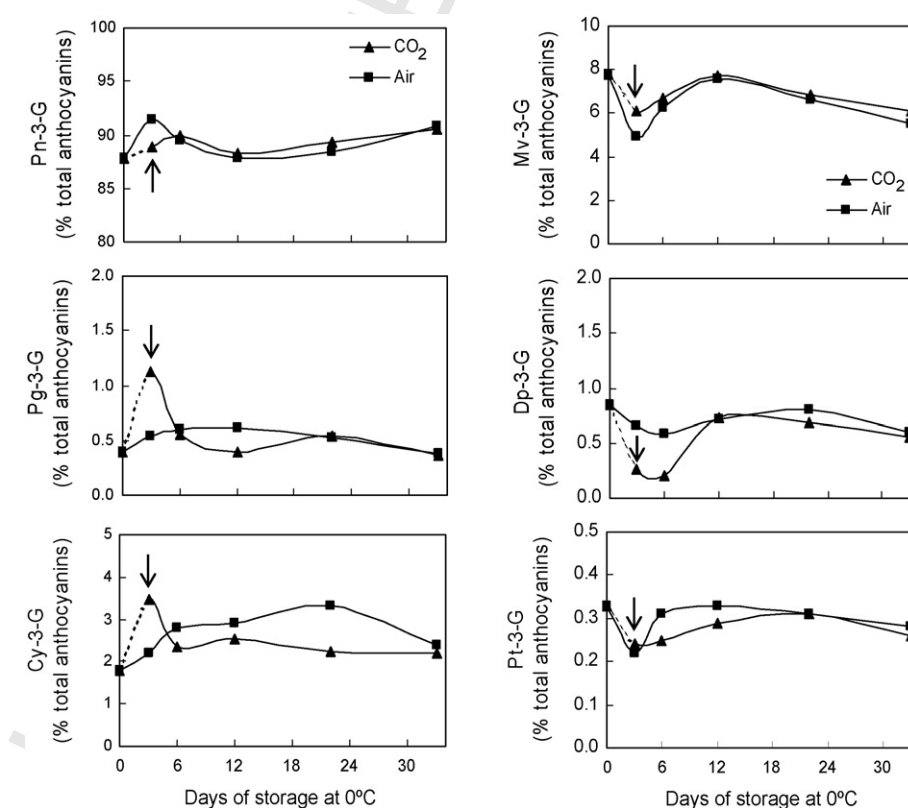


Fig. 3. Percentage of individual anthocyanins relative to the total anthocyanin content in untreated and CO₂-treated cardinal table grapes during storage at 0 °C. The dotted line indicates the short period of high CO₂ treatment and the row indicates the transfer of CO₂-treated fruit to air.

3.3. Skin colour changes in untreated grapes and those exposed to CO₂ during storage at 0 °C

We determined the evolution of the parameters L^* , a^* , b^* , chroma and the hue angle in untreated and CO₂-treated grapes during storage at 0 °C (Fig. 4). The skin of untreated and CO₂-

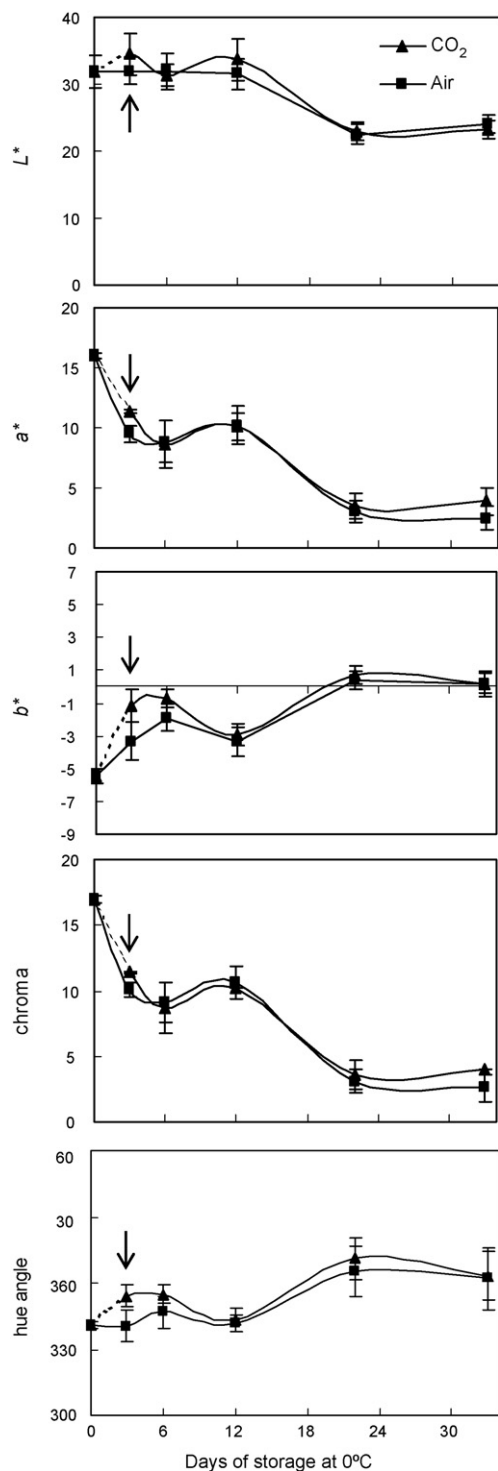


Fig. 4. Evolution of the L^* , a^* , b^* , chroma and hue angle in untreated and CO₂-treated cardinal table grapes during storage at 0 °C. The dotted line indicates the short period of high CO₂ treatment and the row indicates the transfer of CO₂-treated fruit to air. The results are the mean of three replicate samples \pm S.E.

treated berries showed a similar evolution in their red-violet colour during low-temperature storage. The values of parameter a^* and chroma showed a progressive decrease in the first days of storage at 0 °C, and were higher in untreated than in CO₂-treated grapes. This decrease was particularly notable after 22 days when they reached their lowest values. On the contrary, the values of the parameter b^* and the hue angle undergo an opposite effect over the storage period and they were higher in CO₂-treated than in untreated grapes. After 22 days of storage at 0 °C, the values of the parameter b^* and hue angle were very near 0, and the L^* parameter reached minimum values, indicating that at this time the colour of untreated and CO₂-treated berries was dark violet.

3.4. The antioxidant capacity of table grapes in response to low temperature and short-term exposure to high CO₂

The antioxidant capacity of Trolox and reference standard solutions of anthocyanins was determined using the ABTS^{•+} scavenging assay. Inhibition of absorbance at 734 nm was calculated and plotted as a function of the concentration of each compound (Fig. 5). Subsequently, the data were adjusted by linear regression and the slope relation between reference standards and Trolox were used to determine the antioxidant capacity measured as TEAC for individual anthocyanins. A comparison between the antioxidant capacity of the anthocyanins indicated that Dp-3-G had the highest antioxidant capacity (6.99 mM) followed by Pg-3-G (3.68 mM). On the other hand, Mv-3-G had the lowest TEAC value (1.37 mM). According to these TEAC values (mM) and the concentration of the individual anthocyanins (mg/100 g FW), the contribution of the major individual anthocyanins to the TAC value of untreated and CO₂-treated table grapes was calculated (mM TE/100 g FW, Table 3). Our results indicate that after 3 days storage at 0 °C the untreated grapes had the highest anthocyanin content (27.55 mg/100 g FW) and displayed the largest TAC value (52.45 mM TE/100 g FW). Although an increase in each of the anthocyanins contributed to this high TAC value, Pn-3-G was mainly responsible for this sharp early rise in the TAC value of untreated grapes. Pn-3-G had a low average TEAC value (1.73 mM) but its strong contribution could be explained by the drastic increase in the content of this predominant anthocyanin after 3 days in storage at low temperature (Table 3). Conversely, no significant difference was observed in the total TAC value in 3-day CO₂-treated grapes and the Pn-3-G values remained at similar values to those observed in pre-stored grapes. Pg-3-G was present in relatively small amounts in these berries but it had a very high average TEAC value (3.68 mM) and thus, it was an important contributor to the TAC value in CO₂-treated grapes. Additionally, our results indicated that as result of the changes in the concentration of individual anthocyanins, the TAC contribution showed significant changes throughout low-temperature storage (Table 3). The LSD test confirmed that the factors time (D) and time \times CO₂-treatment interaction (D \times T), significantly affected the TAC contribution of individual anthocyanins and the TAC value of untreated and CO₂-treated table grapes ($P < 0.05$). The highest F value for the factor time was found for the contribu-

Table 3
TAC contribution (mM TE/100 g FW) of the individual anthocyanins and calculated TAC value of untreated and CO₂-treated cardinal table grapes during storage at 0 °C

Days	Pn-3-G		Mv-3-G		Cy-3-G		Pg-3-G		Dp-3-G		TAC value ^a	
	Air	CO ₂	Air	CO ₂	Air	CO ₂	Air	CO ₂	Air	CO ₂	Air	CO ₂
0	23.97 ± 5.79	23.97 ± 5.79	1.65 ± 0.15	1.65 ± 0.15	0.84 ± 0.01	0.84 ± 0.01	0.23 ± 0.01	0.23 ± 0.01	0.95 ± 0.11	0.95 ± 0.11	27.63 ± 6.09	27.63 ± 6.09
3	47.27 ± 0.62	24.53 ± 1.57	1.95 ± 0.20	1.30 ± 0.26	1.25 ± 0.25	1.04 ± 0.12	0.58 ± 0.02	0.72 ± 0.03	1.38 ± 0.03	0.30 ± 0.11	52.45 ± 1.12	27.91 ± 2.10
6	28.15 ± 8.14	22.29 ± 5.59	1.56 ± 0.37	1.31 ± 0.28	0.97 ± 0.17	0.65 ± 0.11	0.40 ± 0.04	0.30 ± 0.05	0.75 ± 0.10	0.21 ± 0.04*	31.84 ± 8.83	24.77 ± 6.08
12	19.34 ± 0.10	33.13 ± 5.91	1.31 ± 0.12	2.30 ± 0.08	0.70 ± 0.03	1.05 ± 0.27	0.29 ± 0.03	0.31 ± 0.05	0.63 ± 0.04	1.11 ± 0.33	22.27 ± 0.34	37.89 ± 6.66
22	24.89 ± 3.37	22.24 ± 1.97	1.48 ± 0.20	1.34 ± 0.33	1.02 ± 0.03	0.61 ± 0.03	0.31 ± 0.04	0.29 ± 0.07	0.92 ± 0.06	0.69 ± 0.06	28.61 ± 3.72	25.18 ± 1.97
33	31.94 ± 6.22	37.59 ± 4.51	1.54 ± 0.37	2.01 ± 0.25	0.93 ± 0.11	1.01 ± 0.19	0.29 ± 0.05	0.33 ± 0.05	0.86 ± 0.36	0.92 ± 0.10	35.55 ± 7.12	41.86 ± 5.11
Significance	D*, D × T*		D*, D × T*		D*, D × T*		D*, D × T*		D*, T*, D × T*		D*, D × T*	

* Significant at $R < 0.05$, where D = days and T = CO₂-treatment.

^a TAC value was calculated as the sum of the contribution of individual anthocyanins. The contribution of Pn-3-G to the TAC value is not included.

tion of Pg-3-G TAC (F value = 79.49), followed by Mv-3-G (F value = 15.26). The effect of exposure to high CO₂ throughout low-temperature storage was only significant on the TAC contribution of Dp-3-G. The decrease in the levels of Dp-3-G up to 6 days in storage at 0 °C seemed to explain the significant effect of CO₂ on the TAC contribution of this anthocyanin.

4. Discussion

Cold-stressed growth conditions are known to produce an increase in anthocyanin synthesis, although the mechanisms underlying temperature sensitivity in anthocyanin production are poorly understood (see reviews by Mol et al., 1996; Chalker-Scott, 1999). In general, the effects of low-temperature storage on anthocyanin production have been assessed in terms of total anthocyanin levels rather than changes in the levels of specific anthocyanins. In the present work, we have identified the individual anthocyanin pigments in Cardinal table grapes using mass spectrometry and we have examined the effects of low temperature (0 °C) with and without high CO₂ (20%) on each of these. Moreover, instead of relative peak areas, the precise determination of the concentration of the individual anthocyanins in this variety has been calculated. We identified six anthocyanins and in contrast to wine grapes in which the main anthocyanin has been reported to be Mv-3-G (Muñoz-Espada et al., 2004), Pn-3-G was the predominant anthocyanin in the skin of table grapes. It is also important to note the presence of Pg-3-G in the skin of Cardinal table grapes. The presence of 3-*O*-glucoside of pelargonidin was also previously found in Concord, Rubired, and Salvador grape juices. Rubired and Salvador grapes are hybrids from *V. vinifera* and *Vitis rupestris* and Concord is a grape from the native American cultivar *Vitis labrusca* (Wang et al., 2003). The amount of the six anthocyanins found in untreated grapes all increased after storage for 3 days at 0 °C. In accordance with the anthocyanin biosynthetic pathway in plants (Schijlen et al., 2004; Winkel-Shirley, 2001; Stiles et al., 2007), we suggest that the cyanindin, delphinidin and pelargonidin branches seem to be involved in anthocyanin accumulation during the first days of storage at 0 °C. Although further work is needed to know the mechanism implicated in the induction of anthocyanins in grapes at very low temperature, our results indicate that at least one of the temperature control points could be upstream of dihydrokaempferol, where this branching occurs. This is consistent with the induction of *PAL* and *CHS* mRNA in untreated grapes after 3 days at 0 °C (Sanchez-Ballesta et al., 2007), which may lead to increased upstream enzyme activity. In contrast, short-term exposure to high CO₂ levels (20% for 3 days) had no significant effect on anthocyanin content as the observed values were similar to those in pre-stored grapes. Moreover, in grapes treated for 3 days in CO₂ the increase in pelargonidin, an anthocyanin synthesized directly from dihydrokaempferol, was concomitant with the decrease in anthocyanins synthesized directly from dihydromyricetin, namely delphinidin, petunidin and malvidin. It is known that the anthocyanin biosynthesis pathway is controlled in response to different developmental and environmental cues (Holton and Cornish, 1995; Mol et al., 1998). Another challeng-

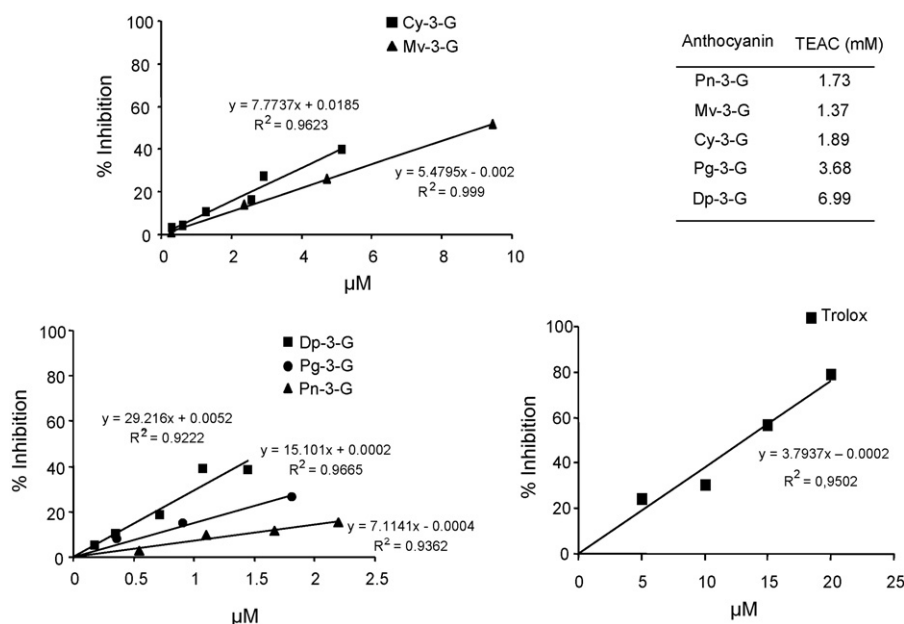


Fig. 5. Antioxidant capacity of Trolox and standard reference anthocyanin solutions using the ABTS^{•+} scavenging assay. The TEAC values (mM) were calculated from the standard and Trolox slope ratios.

ing aspect would be to clarify the detailed course of the reactions and control systems involved in the effects of low temperature and high CO₂ on anthocyanins biosynthesis in fruit tissues.

Anthocyanins are the most prominent pigments in grape skin and they are strong antioxidants. Their double bond conjugate systems allow electron delocalization, resulting in very stable structures and a powerful antioxidant activity. Furthermore, the extent and position of hydroxylation and methoxylation in the B ring modulates their stability and reactivity (Muñoz-Espada et al., 2004). Differences in antioxidant activities between various anthocyanins have been noted in several studies (Tsuda et al., 1994; Wang et al., 1997; Deighton et al., 2000). Moreover, the increase in anthocyanin content in table grapes measured by the pH differential method was not always associated with a similar proportional increase in antioxidant capacity measured by ABTS assay (Sanchez-Ballesta et al., 2007). It has been reported that pH differences have a major influence on scavenging capacity of wine anthocyanins (Borkowski et al., 2005) and that the presence of acid in the solvent has a influence negative in the antioxidant capacity of samples measured by ABTS procedure (Pérez-Jiménez and Saura-Calixto, 2006). In the present work we decided to calculate the TAC value of the samples considering the contribution of individual anthocyanins to the TAC on the basis of their concentration and antioxidant capacity. We found that the calculated TAC values were higher in untreated grapes stored for 3 days at 0 °C than in pre-stored grapes. The rise in Pn-3-G levels, the predominant anthocyanin in this variety, contributed to the peaking of TAC value in grapes at the beginning of low-temperature storage. Moreover, the fact that the calculated TAC values were lower in grapes treated with CO₂ seems to be due to the maintenance of Pn-3-G levels.

We suggest that the accumulation of anthocyanins at the beginning of storage at 0 °C may be a response to a burst in free radicals originated by the fruits' own metabolism in response to

the temperature shift. At this low temperature, the untreated fruit triggers this natural antioxidant defense mechanism to reduce the severity of stress. Since the calculated antioxidant capacity in our CO₂-treated table grapes was similar to that found in pre-stored grapes, we can conclude that CO₂ reduces the sensitivity of these grapes to low temperature rather than activating this defense mechanism. In this sense, we previously reported that the effectiveness of this gaseous treatment was not mediated by the induction of either *STS* gene expression (Sanchez-Ballesta et al., 2006) or that of PR genes (Romero et al., 2006). Indeed, a decrease or no change in antioxidant activity was reported in fruits stored at low temperature under controlled atmospheric conditions (Van der Sluis et al., 2001). Our results indicate that after prolonged low-temperature storage similar calculated TAC values were obtained from untreated grapes and those exposed to short-term high CO₂.

The colour of red and black grapes results from the accumulation of the corresponding pigments, the orange to red pelargonidin, the red to magenta cyanidin, and the violet to blue delphinidin. Each variety of grapes has a unique set of anthocyanins (Mazza and Miniati, 1993) and the external colour of the skin of the grapes is used to classify grape varieties into the following groups: green-yellow, pink, red, red-grey, red-dark violet, red-black and blue-black. The mature berries of cardinal table grapes usually possess red or violet tones of greater or lesser intensity, and the amount and nature of its anthocyanins could situate this variety in the red-black group (Carreño et al., 1997). These authors also reported that the *L** hue angle and chroma values in grapes with violet tints were closely correlated, both between each other and also with the visual color, while the value of *a** was not a representative parameter of color. Taking into account the results obtained here, it seems that the most significant differences in the *L*, chroma and hue angle values between untreated and CO₂-treated grapes appear during the

initial days of storage at 0 °C. The fact that the reduction in the blue tones was greater in CO₂-treated than in untreated grapes in the first 6 days of storage at 0 °C could be associated with the decrease in the amount of delphinidin pigments. However, the possible relationship between colour and the changes in the levels of Dp-3-G and Pg-3-G after exposure to high CO₂ levels should be further studied. After 22 days storage at 0 °C, the colour of untreated and CO₂-treated berries becomes dark violet with red-violet tints of lesser intensity. At this time, the *L**, *b**, chroma and hue angle values are in accordance with those reported by Carreño et al. (1997) for ripe dark violet grapes.

Until now, the presence of anthocyanins characteristic of any particular species has been useful in testing or confirming the interspecies origin of the genotypes that produce the characteristics of grapes and blackberries. The data we have obtained provide a new framework for the effect of high CO₂ treatment and low temperature on the induction of specific anthocyanins in table grapes. Furthermore, the present results show that the analysis of the profiles of individual anthocyanins and their contribution to the TAC value represents a valuable tool to define their tolerance to specific environmental storage conditions.

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Discusión

1. Evolución de la calidad de uvas conservadas con altos niveles de CO₂ y bajas temperaturas.

Uno de los objetivos de este trabajo ha sido estudiar la eficacia del pretratamiento con altas concentraciones de CO₂ en el mantenimiento de la calidad de los diferentes tejidos de uva durante su conservación a bajas temperaturas (0°C). Los parámetros de calidad se analizaron a lo largo del periodo de conservación en frutos tratados y no tratados, coincidiendo con el muestreo realizado al finalizar el tratamiento gaseoso (3 días con 20% CO₂) y durante su posterior transferencia al aire.

1.1. Parámetros de calidad de la baya.

La aplicación de altos niveles de CO₂ durante 3 días a bajas temperaturas no modificó el contenido de sólidos solubles (SSC) ni el pH del zumo, observándose valores similares a los cuantificados en los frutos recién cosechados. Por el contrario en los frutos no tratados y mantenidos en aire durante 3 días a 0°C se observó un aumento significativo en los valores de SSC y pH, coincidiendo con una disminución en la acidez titulable (TA). Después de 6 días de conservación estas diferencias en los parámetros de calidad entre uvas tratadas y no tratadas fueron menos notables. Asimismo, al final del periodo de conservación no se observaron diferencias significativas en cuanto al contenido de SSC entre uvas tratadas y no tratadas, aunque en ambos casos aumentó significativamente con respecto a los frutos recién cosechados. Estos cambios en el contenido de SSC y TA por efecto de la interacción bajas temperaturas-alto CO₂ se vieron reflejados en la evolución del índice de madurez (SSC/TA), el cual fue menor en uvas tratadas con CO₂, indicando que el tratamiento gaseoso redujo los cambios metabólicos durante la conservación. Se ha descrito que los valores de SSC, TA y pH permanecen constantes en distintas variedades de uva almacenadas a 0°C bajo diferentes CA (Crisosto et al., 2002; Artés-Hernández et

al., 2006). Resultados similares se obtuvieron en uvas Muscadine almacenadas durante 24 días a 0, 4,5 y 20°C (Takeda et al., 1983). Sin embargo, en uvas de mesa Flame se observó un incremento en el contenido de SSC de 2,5 °Brix después de 4 días a 1°C, mientras que en uvas almacenadas bajo condiciones de MAP durante el mismo periodo de tiempo el incremento en los valores de SSC fue de 1 °Brix (Martínez-Romero et al., 2003). Respecto a las modificaciones de la textura durante los primeros días de conservación no se observaron diferencias significativas en la firmeza de las uvas tratadas con alto CO₂ con respecto a los frutos recién cosechados. En trabajos previos se ha descrito la eficacia de las altas concentraciones de CO₂ en el mantenimiento de la firmeza de la chirimoya durante el proceso de maduración a 20°C (Del Cura et al., 1996), y de la adhesión celular durante la conservación a temperaturas de daño por frío (Maldonado et al., 2002). En tomates pretratados con altos niveles de CO₂ también se observó un mantenimiento de la firmeza debido al efecto del CO₂ bloqueando la acumulación de mensajeros de genes implicados en los principales cambios de la maduración, entre los que se encuentra el gen de la poligalacturonasa (Rothan et al., 1997).

Respecto al color, comparando los frutos tratados y no tratados, los cambios más notables en los parámetros *L**, croma y ángulo hue se observaron al finalizar el tratamiento gaseoso de 3 días. Concretamente en los frutos tratados con CO₂ se observó un menor descenso en los valores de los parámetros de color analizados y un incremento en el ángulo hue. El valor de croma en la piel de las bayas tratadas y no tratadas disminuyó progresivamente durante el periodo de conservación alcanzándose valores mínimos después de 22 días de conservación. Se ha descrito previamente que la disminución en los parámetros implicados en el color, cuando el color visual de las uvas era más intenso, podría ser atribuida al hecho de que las uvas pasaban a ser más oscuras al adquirir una coloración violeta oscuro (Carreño y Martínez, 1995). Resultados similares en el color han

sido descritos en uvas de mesa cv. Autumn seedless tras 60 días de conservación en CA (5 kPA de O₂+15 kPA de CO₂) a 0°C (Artés-Hernández et al., 2004). Distintos estudios demuestran la importancia del color como indicador de la calidad, y por tanto, de la aceptabilidad del fruto (Clydesdale, 1993). Según Carreño et al. (1997) las uvas de mesa cv. Cardinal podrían estar incluidas en el grupo de las uvas rojas-negras por la cantidad total de antocianos y naturaleza del antociano mayoritario. Además de la variedad, las condiciones agronómicas y culturales influyen en los perfiles de antocianos afectando al color de la uva (Mazza y Maniati, 1993). En este trabajo se han observado ligeras variaciones en el valor del ángulo hue, uno de los parámetros más representativos de la apariencia visual de la piel de uvas de esta variedad, tanto en frutos tratados como no tratados con CO₂ que podrían estar relacionadas con los cambios en el perfil de antocianos analizados.

Por último, no se observó oscurecimiento en la pulpa de la uva ni se apreciaron olores ni sabores anómalos, que podrían haberse producido como consecuencia de posibles procesos fermentativos a lo largo del periodo de conservación. Estos resultados son muy positivos, ya que se han observado este tipo de efectos indeseables desde el inicio de la aplicación de CA en distintos frutos (Uota, 1957; Crisosto et al., 2002,b; Kader, 2002).

1.2. Parámetros de calidad asociados al racimo.

El oscurecimiento y marchitamiento del raquis influyen en la apariencia visual de los racimos y ambos parámetros pueden llegar a determinar el periodo máximo de conservación de la uva de mesa. Se ha descrito que distintas concentraciones de CO₂, independientemente de los niveles de O₂, afectan al oscurecimiento del raquis. Así, tras un periodo de conservación de 1 a 2 meses utilizando concentraciones de CO₂ de 10 kPa se observó un mayor oscurecimiento del raquis en las uvas Redglobe cosechadas

tempranamente, mientras que las cosechadas tardíamente toleraron hasta 15 kPa de CO₂ antes de comenzar a mostrar oscurecimiento del raquis en el segundo mes de almacenamiento (Crisosto et al., 2002). En los ensayos realizados en este trabajo se ha observado que los racimos de uva cv. Cardinal toleraron pretratamientos de hasta 20 kPa sin mostrar síntomas de oscurecimiento a los 33 días de conservación. Por el contrario, en los racimos almacenados en aire durante 33 días a 0°C se observó un considerable deterioro en la apariencia visual de los mismos. El efecto beneficioso del pretratamiento con CO₂ en la apariencia de los racimos podría ser explicado por la menor pérdida de agua observada en el raquis de las uvas sometidas a este tratamiento. Se midió el contenido relativo de agua (RWC, del inglés *Relative Water Content*) durante el periodo de conservación y se observó que este parámetro disminuyó significativamente en el raquis de los racimos no tratados como resultado del almacenamiento a 0°C. Distintas especies de plantas sometidas a condiciones de estrés hídrico muestran una disminución en el RWC (Nagy et al., 1995; Walter et al., 1990) que parece estar relacionado con la actividad metabólica del tejido (Flower and Lidlow, 1986). Asimismo, se observó que la pérdida de peso en los racimos de uvas tratadas con CO₂ fue menor que en uvas no tratadas después de 33 días de almacenamiento (3,93% y 7,42% respectivamente). Esta menor pérdida de peso observada en los racimos tratados con CO₂ podría indicar una menor actividad metabólica de los mismos bajo el tratamiento gaseoso, coincidiendo con un retraso del proceso de envejecimiento del raquis. En este sentido se ha observado que tejidos fotosintéticos de frutos tratados con alto CO₂ mantienen mejor su maquinaria fotosintética, al evitar la degradación de clorofilas totales y la pérdida de proteínas solubles del cloroplasto (Merodio et al., 1998).

Por tanto, a la vista de estos resultados, se podría concluir que el pretratamiento de 3 días con altos niveles de CO₂ es adecuado para mantener la calidad de la uva de mesa.

Los resultados obtenidos en relación a este mantenimiento son similares a los descritos para diferentes variedades de uva tratadas con atmósferas ricas en CO₂ (Crisosto et al., 2002; Artés-Hernández et al., 2004). En estudios previos, Yahia et al. (1983) así como Berry y Aked (1997) ya describieron distintos efectos beneficios del tratamiento de uvas con CO₂, tales como retraso de la senescencia, disminución de la respiración de la baya y del raquis, reducción del oscurecimiento del raquis, mantenimiento de la firmeza de la baya, y retraso de la podredumbre. Sin embargo, la formación de sabores anómalos y el oscurecimiento de la baya fueron problemas derivados del tratamiento gaseoso (Kader, 2002).

2. Aislamiento y caracterización de los genes que codifican las principales enzimas implicadas en la ruta de los fenilpropanoides (PAL, STS, CHS).

Con el fin de estudiar el efecto del pretratamiento con altos niveles de CO₂ así como las bajas temperaturas de conservación sobre enzimas clave de la ruta de los fenilpropanoides (PAL, CHS y STS), se aislaron cDNAs parciales de las mismas a partir de la piel de uvas de mesa.

El cDNA parcial *VcPAL* codificó un polipéptido de 222 aminoácidos (aa) que presentó elevados niveles de identidad con la secuencia de *V. vinifera* cv. Lambrusco (Sparvoli et al., 1994) y con otras especies de plantas. El cDNA parcial *VcCHS* de 634 pares de bases (pb) codificó un polipéptido de 211 aa y presentó más del 90% de identidad con tres CHS de distintas variedades de *Vitis* depositadas en las bases de datos, mostrando mayor homología con CHS2 de *V. vinifera* cv. Cabernet Sauvignon (Goto-Yamamoto et al., 2002). Por otro lado, la secuencia parcial del cDNA *VcSTS*, de 773 pb, codificó un polipéptido de 257 aa que compartió niveles significativos de identidad con secuencias de STS de *Vitis* (Melchior and Kindl, 1990; Wiese et al., 1994).

La conservación a 0°C durante 3 días incrementó la abundancia de los transcritos *PAL*, *STS* y *CHS* en la piel de uvas no tratadas, pero estos niveles disminuyeron después de 6 días. Al finalizar los 3 días de tratamiento con CO₂ a 0°C, los niveles de mRNA de *PAL*, *STS* y *CHS* fueron menores que en los frutos no tratados y prácticamente indetectables cuando los frutos se transfirieron al aire a la misma temperatura. En tejidos fotosintéticamente activos, como las hojas de *Arabidopsis thaliana*, los mRNAs de *PAL* y *CHS* se acumularon a bajas temperaturas de manera dependiente de luz (Leyva et al., 1995). Los resultados obtenidos en este trabajo utilizando frutos almacenados en oscuridad, indican que las bajas temperaturas pueden por sí mismas inducir la expresión de estos genes de la ruta de fenilpropanoides en uva. Christie et al. (1994) demostraron que genes de la ruta de biosíntesis de antocianos, como son la *PAL* y *CHS*, pueden ser considerados genes *COR*, regulados por las bajas temperaturas. También se han observado incrementos en la actividad PAL en respuesta a bajas temperaturas en distintas especies (Tan, 1980; Graham y Patersson, 1982). Aunque las uvas cv. Cardinal no mostraron daños durante la conservación a bajas temperaturas, la activación de la expresión de genes de la ruta de los fenilpropanoides los primeros días de almacenamiento a 0°C podría ser consecuencia de la percepción del fruto de esta baja temperatura, inferior a su óptima de conservación. Asimismo, la atenuación de los cambios en la expresión génica en la fase inicial de la conservación a 0°C en los frutos tratados con alto CO₂ podría ser debido al efecto protector del pretratamiento gaseoso.

Los niveles de los mRNAs de la *PAL*, *CHS* y *STS* fueron estudiados periódicamente hasta el final de la conservación en frutos tratados y no tratados. El pretratamiento con alto CO₂ redujo el incremento de los transcritos de *PAL* y *STS* observado en uvas no tratadas, y el máximo en la expresión génica se observó a los 28 días de almacenamiento. Sin embargo, la *CHS* presentó una menor acumulación de mensajeros que *PAL* y *STS* tanto en

uvas tratadas como en no tratadas; aunque, al igual que éstas, el máximo se observó a los 28 días y el CO₂ actuó disminuyendo los niveles del transcrito respecto de las uvas mantenidas en aire desde el comienzo de la conservación. La expresión de los genes *PAL* y *CHS* está regulada por distintos estreses entre los que se encuentran, las bajas temperaturas, el ataque por patógenos y el daño mecánico (Leyva et al., 1995; Seki et al., 2002; Sanchez-Ballesta et al., 2000). Se ha considerado que el incremento en la actividad de la enzima PAL, junto con el de otras enzimas involucradas en la biosíntesis de fenilpropanoides, es un mecanismo de defensa que opera en distintas especies vegetales sometidas a distintos estreses (Dixon y Pavía, 1995). En cultivos celulares de *V. vinifera* infectados por *B. cinerea* se observó el descenso en la síntesis de proteínas totales y la acumulación específica de un número pequeño de proteínas involucradas en resistencia inducida, entre las que se encontraban principalmente las enzimas PAL y STS (Liswidowati et al., 1991). En las uvas no tratadas, los mRNAs de *STS*, *PAL* y *CHS* se acumularon principalmente a los 28 días coincidiendo con la mayor infección por hongo de las uvas. La inducción de estilbenos en respuesta al ataque por patógenos ha sido descrita previamente (Sarig et al., 1997). Los estilbenos son compuestos activos biológicamente con actividad antifúngica frente a distintos patógenos de plantas entre los que se encuentra *B. cinerea* (Adrian et al., 1998). Sin embargo, el pretratamiento con altos niveles de CO₂ parece tener un claro efecto inhibitor sobre la inducción de la expresión del gen *STS* durante la conservación de la uva de mesa. Así, el ligero aumento de los niveles del transcrito *STS* observado en los frutos tratados respecto a los niveles encontrados en las uvas recién traídas de campo, se mantuvo estable hasta el final del almacenamiento y fue, en todo caso, menor que el observado en uvas no tratadas, al igual que el porcentaje de ataque por hongos. Estos resultados indican que la eficacia del pretratamiento con CO₂

reduciendo el ataque por hongo durante la conservación a bajas temperaturas parece no estar mediada por la inducción de la expresión de los genes *PAL*, *STS* y *CHS*.

3. Contenido de resveratrol en los extractos de piel de uva.

La concentración de resveratrol en las uvas es muy dependiente del cultivar. En uva de mesa cv. Cardinal, los cambios observados en los niveles de mRNA *STS* fueron paralelos al contenido de *trans*-resveratrol al final del periodo de conservación, demostrando que la acumulación de estilbenos en la piel de las bayas está altamente regulada a nivel de la expresión génica de *STS*. Además, en frutos no tratados se observó que la acumulación de *trans*-resveratrol acompañó al incremento en el porcentaje de ataque por hongos observado al final de la conservación a 0°C. La producción de fitoalexinas de la familia del estilbeno, es una de las rutas de defensa más importantes en uva (Langcake y Pryce, 1977). Se ha descrito que el resveratrol se acumula en respuesta a estreses bióticos y/o abióticos como: infección por patógenos, radiación UV, o sustancias químicas (Langcake, 1981; Creasy y Coffee, 1988; Jeandet et al., 1995; Sarig et al., 1997; Cantos et al., 2002). Desde que se describió que *B. cinerea* puede actuar como elicitador de la producción de *trans*-resveratrol en vid (Langcake y Pryce, 1976), distintas investigaciones se han dirigido hacia la interacción de este huésped-patógeno (Jeandet et al., 1995; Adrian et al., 1998; Breuil., 1998). Además, esta fitoalexina también ha recibido en los últimos años mucha atención por su implicación en la salud humana (Jang et al., 1997; Hung et al., 2000; Whitsett y Lamortiniere, 2006).

Por otro lado, durante la primera fase de conservación a 0°C se observó un descenso de los niveles de *trans*-resveratrol, que fue mayor en los frutos tratados con CO₂ al finalizar los 3 días de tratamiento. Es posible que la disminución en los niveles de *trans*-resveratrol fuese el resultado de la unión de subsecuentes moléculas de *trans*-resveratrol

oxidadas dando lugar a la formación de distintos oligómeros, tales como ϵ y α -viniferinas (Langcake y Pryce, 1977); pero, hasta el momento, se desconoce la causa de la misma. Tras la transferencia al aire de los frutos tratados con altos niveles de CO_2 , se observó un aumento paulatino del contenido de *trans*-resveratrol hasta los 33 días de conservación, alcanzando niveles similares a los cuantificados en los frutos recién cosechados.

Durante el periodo de vida útil, cuando las uvas son transferidas a 20°C , el aumento en el contenido de *trans*-resveratrol fue de un 72% en las uvas tratadas, mientras que sólo aumentó un 10% en las no tratadas. El alto potencial para sintetizar *trans*-resveratrol de las uvas tratadas con CO_2 durante el periodo de vida útil fue similar al de los frutos no tratados al final del almacenamiento a 0°C . También se ha descrito previamente, un aumento en el contenido de *trans*-resveratrol durante el periodo de vida útil de uvas de mesa almacenadas en CA (Artés-Hernández et al., 2003). Este mayor incremento en los niveles de *trans*-resveratrol coincide con el mayor porcentaje de ataque por hongo, corroborando, una vez más, la relación existente entre la podredumbre y el contenido en *trans*-resveratrol.

4. Antocianos totales y capacidad antioxidante de la piel de uva de mesa conservada a 0°C y altos niveles de CO_2 .

Se analizó la evolución del contenido de antocianos a lo largo de la conservación de las uvas tratadas y no tratadas, así como la capacidad antioxidante de la piel de las mismas, donde se encuentran principalmente estos compuestos.

En los frutos no tratados se observó un incremento transitorio en el contenido de antocianos totales los primeros días de conservación a 0°C . La aplicación de un 20% de CO_2 evitó este incremento inicial en el contenido de antocianos totales, y únicamente después de la transferencia al aire se alcanzaron valores similares a los cuantificados en frutos no tratados. A lo largo de los muestreos realizados durante la conservación, se

observó una disminución en el nivel de antocianos totales, tanto en uvas tratadas como no tratadas, respecto de los valores de los primeros días de almacenamiento; siendo en todo caso estos niveles superiores a los observados en los frutos recién traídos de campo. Se sabe que la síntesis de antocianos continúa después de la cosecha y también durante la conservación a bajas temperaturas (Kacperska, 1989; Christie et al., 1994; Solecka et al., 1999). Además, Roubelakis-Angelakis y Kliwer (1986) observaron un aumento en la actividad PAL paralela a la acumulación de antocianos durante la maduración de uvas de mesa cv. Cardinal. También se ha descrito un aumento del metabolismo fenólico y de la capacidad antioxidante en espinacas como respuesta a estreses bióticos y abióticos (Howard et al., 2002). Durante los primeros días de almacenamiento se observó un aumento de la capacidad antioxidante, determinada por el método ABTS, en uvas no tratadas que coincidió con el incremento en el contenido de antocianos totales citado anteriormente, aunque no en la misma proporción. Así, mientras que el aumento de la capacidad antioxidante fue de un 20%, los antocianos aumentaron hasta un 62%. Por otro lado, en los frutos tratados con alto CO₂ el ligero incremento en el contenido de antocianos observado al finalizar el tratamiento gaseoso fue asociado a un descenso de un 30% en la capacidad antioxidante respecto de los frutos recién traídos de campo. Este efecto se mantuvo tras la transferencia al aire de la uva, aunque a medida que se perdía el efecto del CO₂ la capacidad antioxidante fue aumentando. También se ha descrito una disminución de la capacidad antioxidante de espinacas frescas cortadas almacenadas a 10°C en MAP (Gil et al., 1999). Al final de la conservación, la capacidad antioxidante de las uvas no tratadas disminuyó mientras que las tratadas con CO₂ mantuvieron valores similares a los frutos recién traídos de campo. Algunos autores, como Kalt et al. (1999) y Wang y Lin (2000) encontraron una correlación significativa entre la capacidad antioxidante, fenoles totales y antocianos. Por otro lado, algunas investigaciones han indicado que los antocianos

podrían ser menos significativos en la correlación con las propiedades antioxidantes de los frutos (Arnous et al., 2002; Kallithraka et al., 2005). Orak et al. (2007), analizaron las correlaciones existentes entre capacidad antioxidante, fenoles totales y antocianos en distintos cultivares de uva tinta y concluyeron que la capacidad antioxidante determinada en estas bayas no siempre está relacionada con el contenido en antocianos.

5. Identificación y cuantificación de los principales antocianos presentes en la piel de uva. Capacidad antioxidante de los antocianos cuantificados.

Se identificaron y cuantificaron mediante HPLC-DAD-MS seis antocianos monoglucósidos, incluyendo la pelargonidina-3-G. Aunque se había identificado la presencia de pelargonidina-3-G en zumos de uva obtenidos de los cultivares híbridos de *V. labrusca* y *V. rupestris* (Wang et al., 2003), es la primera vez que se describe la presencia de este antociano en frutos de *V. vinifera* contrariamente a lo observado por Carreño et al., (1997). Por otro lado y coincidiendo con estos autores, la peonidina-3-G es el antociano predominante en la piel de uva de mesa cv. Cardinal. La conservación a 0°C durante los 3 primeros días incrementó la concentración de cada una de los seis antocianos identificados. Es importante destacar el gran incremento en el contenido de peonidina-3-G (+97%), alcanzando valores de 25,20 mg/100 g peso fresco y de pelargonidina-3-G (+141%), que pasó de 0,061 a 0,147 mg/100 g peso fresco. El incremento fue menos pronunciado en cianidina-3-G (+49%), delphinidina-3-G (+48%) y petunidina-3-G (+25%), siendo moderado en malvidina-3-G (+18%). De acuerdo con la ruta biosintética de antocianos en plantas (Schijlen et al., 2004, Winkel-Shirley, 2001; Stiles et al., 2007), y considerando los cambios mencionados en los antocianos identificados en esta variedad, se sugiere que, en los frutos después de 3 días de almacenamiento en aire a 0°C, se activan las tres vías de síntesis de los antocianos derivados de la cianidina, delphinidina y pelargonidina. Estos

resultados apuntan a que, al menos un punto de control de la temperatura en la ruta de biosíntesis de antocianos está por encima del punto de ramificación. Esto es consistente con la inducción de los mRNAs de *PAL* y *CHS* observada en uvas no tratadas después de 3 días a 0°C, lo que podría conducir a un aumento de las actividades enzimáticas antes del punto de control de temperatura previamente citado.

Mientras que el contenido de antocianos en los frutos no tratados alcanzó su máximo (27,55 mg/100 g peso fresco) después de 3 días a 0°C, al finalizar el tratamiento gaseoso los niveles fueron similares a los de los frutos recién cosechados. Además, la exposición durante 3 días a un 20% de CO₂ no modificó el contenido de peonidina-3-G (0%); incrementó el de cianidina-3-G (+24%) y pelargonidina-3-G (+200%), al tiempo que descendió el de delphinidina-3-G (-64%), malvidina-3-G (-21%) y petunidina -3-G (-27%). Estos resultados apuntan hacia un diferente control del alto CO₂ y las bajas temperaturas sobre la ruta de síntesis de los antocianos.

Los resultados sobre el efecto de la temperatura y el CO₂ en la concentración y perfiles de los antocianos en uva de mesa durante su conservación postcosecha, son acordes con los descritos previamente por Holton y Cornisa (1995) y Mol et al. (1998); donde se indica que la ruta de biosíntesis de los antocianos es controlada en respuesta a diferentes estreses ambientales así como durante la etapa de crecimiento y desarrollo del fruto. Al final de la conservación, los valores de los antocianos fueron, en general, superiores a los obtenidos en los frutos recién traídos de campo, siendo la peonidina-3-G la que presentó el mayor aumento a los 33 días de conservación; alrededor de un 44% en frutos no tratados y de un 70% en frutos tratados. Sin embargo, las excepciones fueron la delphinidina-3-G y la malvidina-3-G que no aumentaron y mantuvieron valores similares a los de los frutos recién cosechados.

En base a la aparente falta de unanimidad en la correlación entre los valores de capacidad antioxidante y contenido en antocianos totales, se planteó el cálculo de la capacidad antioxidante total (TAC) de los frutos tratados y no tratados a lo largo de la conservación, teniendo en cuenta la concentración de cada antociano presente en los extractos y su correspondiente capacidad antioxidante. Asimismo, considerando las grandes diferencias en cuanto a los valores de capacidad antioxidante asignados a cada antociano presentes en la bibliografía (Wang et al., 1997; Deighton et al., 2000; Wang y Lewers, 2007), se optó por analizar la capacidad antioxidante de los diferentes antocianos identificados en nuestra variedad a partir del estudio con patrones comerciales de antocianos. Además, para una mayor precisión, la capacidad antioxidante de cada antociano se calculó según el método ABTS utilizando rectas de calibrado realizadas con diferentes concentraciones de patrones. Los resultados obtenidos indicaron que el antociano con mayor capacidad antioxidante, calculado en equivalentes de Trolox (TEAC), fue la delfinidina-3-G (6,99 mM), seguida de la pelargonidina-3-G (3,68 mM), cianidina-3-G (1,89 mM), peonidina-3-G (1,73 mM) y malvidina-3-G (1,37 mM). Estos datos difieren de los observados por Wang et al. (1997), donde se describe que la cianidina-3-G es el antociano con mayor capacidad antioxidante. El estudio comparativo de los valores de TAC entre frutos tratados y no tratados durante su conservación indicó que el valor máximo (52,45 mM TE/100 g peso fresco) lo exhibieron los frutos no tratados después de 3 días a 0 °C. La peonidina-3-G fue la responsable principal de este incremento en el valor de TAC calculado. Aunque el valor de TEAC para este antociano resultó ser intermedio (1,73 mM), su contribución a la TAC podría ser explicada por el importante aumento de su contenido en uvas no tratadas al principio de la conservación. Sin embargo, en las uvas tratadas con CO₂, tanto los valores de peonidina-3-G como de la TAC fueron similares a los encontrados en uvas recién cosechadas. La transitoriedad de los efectos de las bajas temperaturas y el alto CO₂ dio lugar a que las

diferencias en los valores de TAC entre uvas tratadas y no tratadas no fueran significativas al final de la conservación. Además, el estudio comparativo de la TAC calculada a partir de la suma de capacidad antioxidante de cada uno de los antocianos de la muestra, y de la medida a partir de los extractos, nos confirma la infravaloración de la actividad antioxidante empleando el método ABTS, el cual se ve afectado negativamente por pHs ácidos (Pérez-Jiménez et al., 2006). De este modo, se puede concluir que después de 3 días a 0°C el incremento transitorio del contenido de antocianos se correspondía con un aumento también transitorio en su capacidad antioxidante. Estos resultados permiten sugerir que el incremento en la capacidad antioxidante de los frutos podría responder a un estallido en la producción de radicales libres originado por el metabolismo del fruto en respuesta a las bajas temperaturas de conservación. A 0°C, los racimos mantenidos en aire podrían activar su mecanismo de defensa antioxidante para reducir la severidad del estrés causado por los radicales libres. Por el contrario, el mantenimiento de los valores iniciales de TAC en las uvas tratadas con CO₂, permite sugerir que el CO₂ reduce la sensibilidad del fruto a las bajas temperaturas de manera que parece no necesitar activar su capacidad antioxidante. Estas sugerencias se ven apoyadas por los resultados obtenidos de la disminución en la expresión génica de la ascorbato peroxidasa (APX) observada en las bayas tratadas con alto CO₂. El cDNA parcial de la APX, de 539 pb, se obtuvo por RT-PCR y la secuencia deducida de 179 aa presentó el dominio de unión al grupo hemo que comparten todas las proteínas APX, mostrando una elevada identidad con las secuencias de APX citosólicas (82-98%) depositadas en las bases de datos. En cuanto a sus niveles de expresión, la acumulación del transcrito aumentó ligeramente tanto en las uvas tratadas como en las no tratadas, pero se observó un fuerte aumento después de 28 días de conservación en las uvas no tratadas coincidiendo con el mayor desarrollo de podredumbre. Aunque existen distintos estudios sobre APX citosólicas en diferentes

plantas y frutas (Mittler and Zilinskas, 1991; Ishiwaka et al., 1995; Kim y Chung, 1998), no existen estudios acerca del papel del gen *APX* en uva de mesa. Por tanto, los resultados obtenidos donde se muestran diferencias en los mecanismos que operan en las uvas tratadas y no tratadas, conducen hacia la hipótesis de que la enzima APX podría participar eliminando los altos niveles de H_2O_2 existentes en las uvas no tratadas.

Capítulo 2

**Efecto del CO₂ en la mejora de la uva de mesa
con respecto al ataque por hongo. PRs.**

1. Características generales de proteínas relacionadas con la patogénesis (PRs)

Una de las respuestas más frecuentes en las plantas frente al ataque por patógenos es la acumulación de proteínas PRs. En 1971, Abeles et al. sugirieron que las proteínas β -1,3-glucanasa y quitinasa podían participar en la defensa frente a patógenos fúngicos. Por la misma época, las PRs fueron descritas por primera vez como un conjunto original de proteínas que se acumulaban en las hojas de tabaco en relación con la respuesta hipersensitiva a la infección por el Virus del Mosaico del Tabaco (Van Loon y Van Kammen, 1970). Más tarde, se demostró que estas proteínas también eran inducidas por infecciones bacterianas y fúngicas (Redolfi y Cantisani, 1984). Hay distintas observaciones que sugieren un papel defensivo para las proteínas PR como son: la inducción de genes que codifican PRs y proteínas del SAR en plantas como respuesta a subsecuentes infecciones después de una infección necrótica inicial (Kassanis et al., 1974; Van Loon, 1975; Ward et al., 1991); la ausencia de sustrato para una de las proteínas PR (quitinasa) en plantas, pero su presencia en la pared celular de ciertos hongos; así como la actividad antifúngica de quitinasas *in vitro* (Mauch et al., 1988).

Aún no está claro cómo estas proteínas, de forma aislada o combinadas entre sí, pueden participar en la defensa de las plantas frente a la infección por hongos. Se ha propuesto que estas hidrolasas actúan al menos de dos maneras diferentes: directamente, degradando la pared celular del patógeno o indirectamente, promoviendo la liberación de compuestos de la pared celular (oligosacáridos) que pudieran actuar como elicitores de las reacciones de defensa (Meins et al., 1993; Van Loon et al., 1994; Van Loon et al., 2006).

Actualmente se clasifican en 17 familias funcionales que se supone son inducidas como respuesta a infecciones por patógenos (o en situaciones asociadas a la infección), estímulos ambientales o durante el desarrollo (Boller, 1988; Neuhaus, 1999; Van Loon et al., 2006). Durante los últimos años, muchas investigaciones han centrado su interés en

elucidar sus funciones. Específicamente, la principal atención se ha focalizado en el papel fundamental de diferentes quitinasas y β -1,3-glucanasas en la degradación de quitina y β -1,3-glucanos (Aronson, 1965) presentes en la pared celular de patógenos (Mauch et al. 1988). Sin embargo, sólo unas pocas proteínas PR han sido estudiadas a fondo con respecto a sus funciones específicas durante la patogénesis. Esto es debido a la compleja regulación de estas proteínas, ya que aparecen también durante las etapas de desarrollo, y a que algunos centros catalíticos específicos permanecen sin ser todavía identificados (Colditz et al., 2007).

Se ha demostrado que miembros de al menos cuatro de estas familias, como las β -1,3-glucanasas (PR-2), quitinasas (PR-3), proteínas de unión a quitina (PR-4) y proteínas tipo taumatina (PR-5), tienen actividad antifúngica en bioensayos *in vitro*, apoyando el posible papel de estas proteínas en la defensa de plantas (Kombrink y Somssich, 1997).

2. Quitinasas

La importancia de las investigaciones sobre los mecanismos de defensa en plantas ha derivado en un rápido y constante interés por las quitinasas puesto que fueron las primeras proteínas inducidas por patógeno cuya función ha sido identificada. Su sustrato está presente en la pared celular de muchos hongos, insectos, nemátodos, y principales patógenos de las plantas cultivadas (Neuhaus et al., 1987) y, por tanto, son enzimas ubicuas de los mismos. Hidrolizan el enlace β -1,4 entre los residuos de N-acetilglucosamina de quitina, un polisacárido estructural de la pared celular de muchos hongos y del exoesqueleto de invertebrados. Se dividen en dos categorías: exoquitinasas, con actividad sólo en el extremo no reductor de la cadena de quitina; y endoquitinasas, las cuales hidrolizan las uniones internas β -1,4-glicosídicas. Muchas endoquitinasas de plantas, especialmente aquellas con alto punto isoeléctrico, exhiben una actividad lisozima

o tipo lisozima adicional (Collinge et al., 1993; Schultze et al., 1998; Subroto et al., 1999).

Asimismo, en distintas especies de plantas se han encontrado quitinasas ácidas y básicas.

Las quitinasas son enzimas sintetizadas por las plantas en respuesta a estreses bióticos y abióticos como heridas, radiación UV, bajas temperaturas, e invasión de hongos, bacterias y virus (Bowles, 1990; Van Loon et al., 2006). Pueden estar localizadas en distintos tejidos y órganos como semillas (Santos et al., 2004), hojas (Robert et al., 2002), raíces (Lam y Ng 2001), tallos (Lee et al. 2000), flores (Takakura et al., 2000), frutos (Díaz-Perales et al., 1998), tubérculos (Forsyth y Shewry 2002) y bulbos (Yamagami et al., 1998). Son codificadas por un número relativamente pequeño de genes, y la localización de los intrones está bastante conservada. Hasta la actualidad se han encontrado múltiples isoenzimas de quitinasas que han sido divididas en siete clases (I-VII) en base a sus propiedades estructurales (Brunner et al., 1998). Sin embargo, la mayoría de las quitinasas, pertenecen a las primeras cuatro clases (Fig. II)

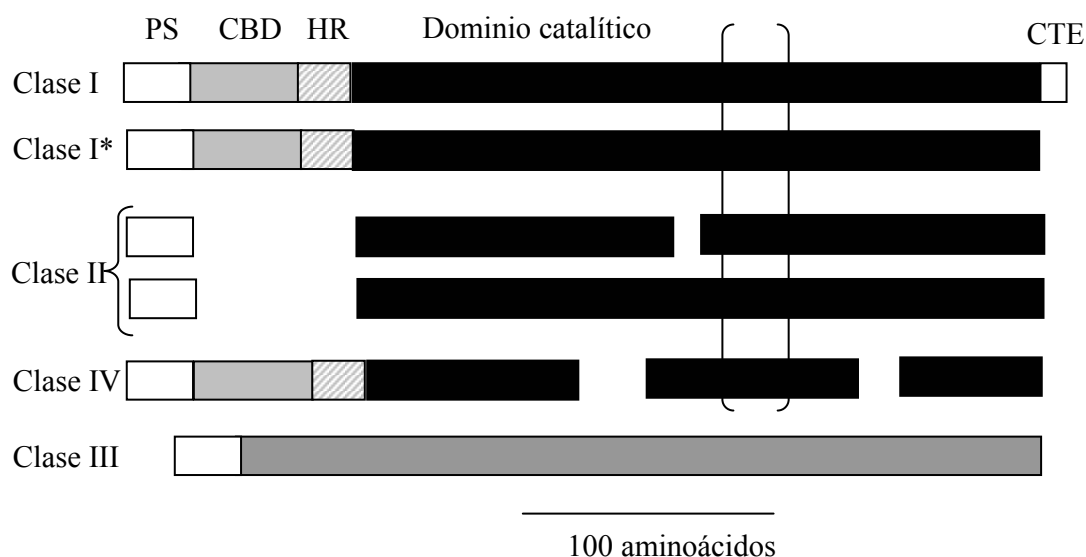


Fig II. Cuadro comparativo de las principales clases de quitinasas (PS: péptido señal; CBD: Dominio de unión a cysteína; HR: región bisagra; CTE: extensión C-terminal)

La familia PR-3 es una familia de quitinasas específica de plantas. Las distintas clases que pertenecen a esta familia han sido definidas primero de acuerdo a la homología de secuencias y a la presencia o ausencia del dominio de unión a quitina (CBD; del inglés *Cysteine-rich chitin-Binding Domain*). Las quitinasas de clase I, II y IV son las más parecidas estructuralmente. Las quitinasas de clase I son sintetizadas como precursores con una secuencia señal N-terminal que las dirige a la ruta secretora. La mayoría de las quitinasas de clase I también presentan un propéptido C-terminal, requerido para su transporte a la vacuola (Neuhaus et al., 1991). La delección de este péptido señal C-terminal redirige a la quitinasa de clase I al apoplasto pero mantiene la actividad enzimática (Grover et al., 2001). Dentro de la proteína madura, el CBD N-terminal, se une al centro catalítico por un espaciador, variable tanto en longitud como en secuencia, pero a menudo rico en prolina o glicina. En el caso de las quitinasas de tabaco, el espaciador se observó que era modificado por hidroxilación de algunas de las prolinas (Sticher et al., 1992). La función de esta modificación no está clara pero puede ser debido a una semejanza de secuencia accidental entre el espaciador y las glicoproteínas ricas en hidroxiprolina secretadas (Neuhaus et al., 1987). En una quitinasa de clase I de tabaco, la delección del CBD y de la región espaciadora, por separado o combinadas, redujo la actividad hidrolítica un 50% y la actividad antifúngica en un 80% (Suárez et al., 2001). Las quitinasas de clase II son generalmente ácidas y extracelulares, y pueden ser detectadas en el fluido apoplástico (Benhamou et al., 1990; Dore et al., 1991). Además, no presentan el CBD ni la región bisagra (HR; del inglés *Hinge Region*) presentes en las quitinasas de clase I. Una posible función de estas quitinasas en la defensa de las plantas es actuar como moléculas señal, eliminando los elicitores procedentes de las hifas del hongo que invaden al huésped, y actuando como una primera línea de defensa (Mauch y Staehelin, 1989). Las de clase III (que pertenecen a la familia PR-8) son hidrolasas extracelulares que no se relacionan

estructuralmente con otras quitinasas de plantas ya que poseen un dominio catalítico conservado que difiere del de las quitinasas de clase I o II (Watanabe et al., 1993). Además, la mayoría se clasifican como quitinasas de clase III en base a su identidad con lisozimas previamente descritas con actividad quitinasa (Graham y Sticklen, 1994). Las de clase IV difieren de la clase I por las delecciones internas existentes entre los dominios de unión a quitina y catalítico. Las quitinasas de clases V y VI fueron definidas en base a la presencia de dos CBDs en tandem, o a la presencia de un CBD truncado y a un largo espaciador rico en prolina, respectivamente. Además, las de clase VI son similares a las quitinasas de bacterias como por ejemplo, *Bacillus circulans*, *Serratia marcescens* o *Streptomyces plicatus* (Melchers et al., 1994). Finalmente, las de clase VII, las últimas detectadas, poseen un dominio catalítico homólogo al de clase IV, pero no presentan el CBD (Punja y Zhang 1993; Neuhaus 1999; Robert et al., 2002).

3. β -1,3-glucanasas

Las β -1,3-glucanasas pertenecen a la familia de proteínas PR-2 y son capaces de catalizar cortes hidrolíticos endógenos en los enlaces β -1,3-glucosídicos de los β -1,3-glucanos, otro de los constituyentes de la pared celular fúngica. Las β -1,3-glucanasas son enzimas muy abundantes, y ampliamente distribuidas en distintas especies de plantas (Meins et al., 1992; Hoj y Fincher, 1995). Aunque el mayor interés radica en el posible papel de las β -1,3-glucanasas en la respuesta de las plantas a patógenos microbianos, hay fuertes evidencias de que estas enzimas también están implicadas en diversos procesos fisiológicos y del desarrollo en plantas no infectadas, incluyendo, división celular, maduración del fruto, respuestas a daño mecánico, bajas temperaturas, ozono y UV-B, entre otros (Waterkeyn, 1967; Fulcher et al., 1976; Hinton y Pressey, 1980; Ernst et al., 1992).

Las β -1,3-glucanasas existen como múltiples isoformas estructurales que difieren en tamaño, punto isoelectrico, estructura primaria, localización celular, y modelo de regulación (Meins et al, 1992; Robinson et al, 1997). La información acerca de las secuencias de estas isoformas está disponible gracias a los cDNAs y clones genómicos de β -1,3-glucanasa de *Nicotiana tabacum*, que constituyen una familia multigénica. Basándose en la identidad de la secuencia de aminoácidos, las distintas β -1,3-glucanasas de tabaco han sido clasificadas en tres clases estructurales (Meins et al, 1992). Se han descrito isoformas con estructuras similares en tomate, patata, melocotón, plátano y otras especies de plantas (Stone y Clarke, 1992; Thimmapuram et al., 2001; Yamaguchi et al., 2002; Receveur-Bréchet et al., 2006).

Las β -1,3-glucanasas son producidas como preproteínas con un péptido señal N-terminal hidrofóbico, el cual es eliminado co-traduccionalmente, y un extremo C-terminal N-glicosilado en un único sitio. Existen evidencias indirectas de que, análogamente con las quitinasas de clase I de tabaco y la lectina de cebada, el extremo C-terminal contenga señales de envío a la vacuola (Worral et al., 1992). Las proteínas de clase I de tabaco son proteínas básicas localizadas en la vacuola celular. Sin embargo, los miembros de la familia PR-2 de clases II y III son secretados al espacio extracelular (Stintzi et al, 1993; Simmons, 1994). En concreto, estas β -1,3-glucanasas de tabaco son proteínas ácidas sin el extremo C-terminal presente en las enzimas de clase I.

Casi todos los genes de β -1,3-glucanasas aislados de especies de plantas contienen un único intron, con la excepción de un gen aislado de *Nicotiana plumbaginifolia* que contiene dos (Castresana et al., 1990). La posición del intrón es la misma en genes de glucanasas ácidas y básicas, indicando que la estructura de los genes de estas glucanasas

está altamente conservada, y que deben haber surgido de un único ancestro común (Linthorst 1991).

4. Regulación génica de quitinasas y β -1,3-glucanasas

Se ha demostrado la existencia de mensajeros secundarios tales como SA, etileno, JA y óxido nítrico en la ruta de señalización que conduce a la activación de genes que codifican proteínas PR (Grant y Loake, 2000; Glazebrook, 2001; Nurnberger y Scheel, 2001; Wendehenne et al., 2001). El SA parece estar involucrado en la inducción de genes asociados con el desarrollo de la SAR. En *Arabidopsis*, se ha identificado un inhibidor llamado NPR1 (del inglés *non-expressed of PR-genes*) que controla la expresión de genes que codifican PRs y que responde a SA y al ataque por patógenos (Cao et al., 1994; Cao et al., 1997). En hojas de arroz, incrementos en los niveles endógenos de SA dieron como resultado una mayor resistencia frente a *Xanthomonas oryzae* y una reducción de las lesiones de la hoja (Babu et al., 2003). El etileno y el JA parecen actuar en rutas diferentes a las del SA conduciendo a la inducción de genes que codifican proteínas PR básicas, tioninas y defensinas (Feys y Parker, 2000; Glazebrook, 2001).

Los genes de quitinasa y β -1,3-glucanasa están regulados a nivel transcripcional. En judía (*Phaseolus vulgaris*), se observó un incremento en la expresión de *pCH18* que codifica una quitinasa de clase I en respuesta al etileno, elicitores de oligosacáridos y patógenos fúngicos (Broglie et al., 1986). Utilizando una construcción quimérica conteniendo la región promotora del gen β -glucoronidasa, Broglie et al. (1989) mostraron que esta región 5' fue suficiente para la expresión regulada por etileno del gen quitinasa en plantas de tabaco. Asimismo, esta sensibilidad al etileno ha sido estudiada también en el promotor de una quitinasa de tabaco de clase I (Shinshi et al., 1995).

La expresión de β -1,3-glucanasas está también regulada por hormonas o en respuesta al ataque por patógenos. Los niveles de mensajero de β -1,3-glucanasa aumentan en respuesta a la hormona etileno (Hart et al. 1993), y ozono (Thalmair et al., 1996); mientras que disminuyen por tratamiento con ABA (Rezzonico et al. 1998) y por combinación de auxinas y citoquinas (Félix y Meins, 1986; Vögeli-Lange et al., 1994). También son inducidas por infecciones con bacterias (Meins y Ahl, 1989), virus (van de Rhee et al., 1993) y hongos (Chang et al., 1992). Sin embargo, algunos genes de β -1,3-glucanasas están únicamente regulados durante el desarrollo y no son inducidos en respuesta a condiciones de estrés, como el gen de la β -1,3-glucanasa aislado del estilo (Ori et al., 1990) y de la antera (Bucciaglia y Smith, 1994) de tabaco.

Existen evidencias de que proteínas quitinasa y β -1,3-glucanasa, de forma individual y particularmente en combinación, pueden ayudar a defender las plantas contra la infección fúngica. Se han realizado análisis con diferentes isoformas de β -1,3-glucanasas y quitinasas para estudiar la actividad antifúngica *in vitro* de estas proteínas y se ha demostrado que quitinasas purificadas de guisante fueron capaces de inhibir el crecimiento de sólo una especie de hongo, mientras que la combinación de quitinasa y β -1,3-glucanasa inhibió el crecimiento de todos los hongos estudiados mostrando actividades sinérgicas entre estas enzimas (Mauch et al., 1988). A partir de este hallazgo, otros estudios han verificado estos resultados en tabaco (Yun et al. 1996), uvas (Derckel et al., 1998) y arroz (Velazhahan et al., 2000). Esto podría indicar que isoformas específicas son inducidas en respuesta a patógenos concretos y sólo ciertas isoformas son capaces de inhibir hongos específicos (Ji et al., 2000; Sela-Buurlage et al., 1993). Por ejemplo, una quitinasa de clase I de tabaco presentó actividad antifúngica frente *Fusarium solani*; pero las quitinasas de clase II mostraron un ligero efecto en la inhibición del crecimiento del

hongo solamente cuando se usaron junto con altas concentraciones de β -1,3-glucanasas (Jach et al., 1995).

Plantas transgénicas de tabaco que expresan β -1,3-glucanasas, especialmente en combinación con una quitinasa, han mostrado mayor tolerancia a patógenos (Jach et al., 1995; Jongedijk et al., 1995). También plantas transgénicas de trigo que sobreexpresaron un gen de quitinasa de clase II (Bliffeld et al., 1999), presentaron mayor resistencia a patógenos fúngicos. Se ha comprobado que las quitinasas de clase I tienen una mayor actividad antifúngica que el resto de quitinasas quizás debido a la presencia del CBD (Sela-Buurlage et al., 1993). Por otro lado, se ha observado que plantas transgénicas que muestran expresión constitutiva de quitinasas exhiben niveles mayores de resistencia a la infección fúngica y retrasan los síntomas de daño frente a patógenos fúngicos (Broglie et al., 1991; Jach et al., 1995; Grison et al., 1996). Plantas de tabaco transformadas con un gen de quitinasa aislado de judía bajo el control del promotor 35S, presentaron una actividad quitinasa hasta 20 veces superior que las plantas control (Broglie et al., 1991).

En 2001, Porat et al. aislaron un cDNA de quitinasa básica de naranja, y comprobaron que su expresión formaba parte de los mecanismos moleculares implicados en la inducción de resistencia del fruto frente a patógenos. Distintas evidencias apoyan el papel antifúngico de las quitinasas de clase I, IV y VI ya que se ha demostrado la habilidad de las mismas para inhibir el crecimiento de las hifas de los hongos *in vitro* (Collinge et al., 1993; Derckel et al., 1998) o *in vivo* en el caso de quitinasas de clase I (Benhamou et al., 1993).

Durante la aclimatación al frío, algunas plantas, incluyendo algunos cereales, secretan proteínas al apoplasto que se adsorben a la superficie de los cristales de hielo extracelular e inhiben o modifican su crecimiento. Estas proteínas son denominadas AFP (del inglés *antifreezing proteins*) (Griffith y Yaish, 2004). En centeno se ha observado que

las AFPs son similares a las PRs de plantas pero se encuentran en complejos oligoméricos (Yu y Griffith, 1999). Asimismo, se confirmó por secuenciación del extremo N-terminal, que algunas de las proteínas abundantes que tuvieron actividad anticongelante *in vitro* eran quitinasas, β -1,3-glucanasas, y proteínas tipo taumatina (Hon, 1994).

Yu et al., (2001) investigaron el papel del SA y del etileno en la inducción de PRs con o sin actividad anticongelante. Mientras que el SA indujo PRs que no tenían actividad anticongelante, el etileno incrementó la acumulación de otras que sí la tenían. Además, sólo algunas isoformas mostraron actividad antifúngica y otras presentaron funciones adicionales como actividad anticongelante (Sela Buurlage et al., 1993; Yeh et al., 2000). Yaish et al. (2006) caracterizaron β -1,3-glucanasas y β -1,3;1,4-glucanasas procedentes de centeno y observaron que eran capaces de inhibir la formación de cristales de hielo, potencialmente fatales para la planta, además de tener actividad enzimática con un papel potencial en resistir la infección por patógenos psicrófilos.

En variedades de *Cynodon* sp. tolerantes a bajas temperaturas se observó un incremento en los niveles de expresión de un gen de quitinasa de clase II (de los Reyes et al., 2001). Además, se ha caracterizado una proteína tipo osmotina (PR-5) aislada de dulcámara (*Solanum dulcamara*) con función crioprotectora (Newton y Duman, 2000). También se ha descrito el papel crioprotector de las PRs en proteínas de la familia PR-2 de tabaco (Hinch et al., 1997), y PR-5 de cacahuete (Dave y Mitra 1998).

Además de las funciones de las quitinasas y β -1,3-glucanasas citadas hasta el momento (como antifúngicas, crioprotectoras y/o anticongelantes) importantes en el mecanismo de defensa de las plantas; la trascendencia de las quitinasas de clase I en los últimos años se debe a que diversos estudios han demostrado que estas proteínas son los principales panalergenos asociados con el síndrome designado látex-fruta (Poley y Slater, 2000). Además de en el látex, se han identificado varias proteínas asociadas a diferentes

PRs en distintos frutos (Receveur-Bréchet et al., 2006). Varios estudios han identificado las quitinasas de clase I como importantes componentes de unión a IgE en suero de pacientes con síndrome de látex-fruta en plátano (Sanchez-Monge et al., 1999), aguacate (Sowka et al., 1998) y castaña (Díaz-Perales et al., 1998). En 2002, O’Riordain et al. clonaron y caracterizaron un alérgeno de *Hevea brasiliensis* que presentó homología con una quitinasa de clase I. La proteína recombinante mostró tener actividad biológica e inmunológica. También se han identificado β -1,3-glucanasas (PR-2) entre los mayores alérgenos responsables de la alergia al látex.

En uva, Robinson et al. (1997) clonaron y caracterizaron dos cDNAs que codifican quitinasa y observaron que la actividad de la misma aumentaba marcadamente al comienzo de la maduración de las bayas y continuaba aumentando durante la fase de acumulación de azúcares. Derckel et al. (1998) caracterizaron isoformas de quitinasa y β -1,3-glucanasas en diferentes estados de maduración de las bayas pero no detectaron actividad glucanasa en ninguno de ellos. Además, añadiendo SA a los racimos infectados por hongo, se observó que sólo se potenciaba la actividad quitinasa de los granos infectados. Busam et al. (1997) observaron que la expresión del gen de una quitinasa de clase III podría servir como un marcador de la SAR en hojas de vid. Por otra parte, existen estudios en granos de uva infectada por *B. cinerea* donde no se han detectado acúmulos de transcritos de quitinasas de clase I en ninguna etapa del desarrollo (Robert et al., 2002), lo que podría indicar que su regulación estuviera relacionada con la temperatura de almacenamiento de la uva.

Con el fin de profundizar en los mecanismos moleculares implicados en la repuesta de uva de mesa a las bajas temperaturas y al tratamiento con altos niveles de CO₂, se estudiarán los niveles de expresión, de actividad, así como las posibles funciones *in vitro* de una quitinasa y de una β -1,3-glucanasa de clase I a lo largo de la conservación de los frutos. Para ello se realizará el aislamiento de genes que codifican una quitinasa y β -1,3-

glucanasa de clase I, así como su expresión heteróloga en *E.coli* para llevar a cabo la caracterización de las proteínas recombinantes.

ARTÍCULO 5

Expression of class I chitinase and β -1,3-glucanase genes and postharvest fungal decay control of table grapes by high CO₂ pretreatment.

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RESUMEN

El efecto del pretratamiento con 20% CO₂ más 20% O₂ durante 3 días fue estudiado con el fin de estudiar su efectividad en el control del ataque por hongo crecido de forma natural durante la manipulación poscosecha y su posible inducción de genes específicos de PRs en uvas de mesa. CDNAs de tamaño completo que codificaban una quitinasa de clase I (*VcCHIT1b*) y una β -1,3-glucanasa (*VcGNSI*) fueron aislados de uvas de mesa (*Vitis vinifera* L. cv. 'Cardinal'). Nuestros resultados indicaron que este pequeño tratamiento con alto CO₂ tuvo un efecto residual y redujo significativamente la incidencia de daño por hongo en uvas de mesa durante el almacenamiento a bajas temperaturas y después de su transferencia a 20°C. Nuestros resultados indican que durante el almacenamiento a bajas temperaturas el patrón de expresión fue diferente entre los genes de las dos PR estudiadas. Así, mientras la abundancia del transcrito *VcGNSI* aumentó fuertemente al comienzo del almacenamiento a 0°C, el aumento de los niveles de mRNA de *VcCHIT1b* fue paralelo al cambio por ataque fúngico. El pretratamiento con altas concentraciones de CO₂ restringió el aumento de la expresión génica de *VcGNSI* y retrasó la acumulación del transcrito *VcCHIT1b* en comparación con uvas no tratadas. Después del paso a 20°C después de 33 días almacenadas en frío, cuando fue observado los niveles máximos de ataque por hongo, hubo un gran aumento en la acumulación de mRNA de *VcCHIT1b* tanto en uvas tratadas como no tratadas, el cual fue mayor en las no tratadas. Nuestros resultados señalan que la expresión de los genes de quitinasa de clase I y de β -1,3-glucanasa no está aumentada en uvas tratadas con CO₂, el cual controla el ataque fúngico. Estos resultados sugieren, entonces, que la eficacia del pretratamiento con altas concentraciones de CO₂ en reducir el ataque por hongo no está mediada por la inducción de los genes de las PRs anteriormente mencionadas.

Expression of class I chitinase and β -1,3-glucanase genes and postharvest fungal decay control of table grapes by high CO₂ pretreatment

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Abstract

The effect of pretreatment with 20% CO₂ plus 20% O₂ for 3 days was studied with regard to its effectiveness on natural postharvest decay control and its possible induction of specific PR genes in table grapes. Full-length cDNAs encoding a class I chitinase (*Vcchit1b*) and β -1,3-glucanase (*Vcgsn1*) were isolated from table grapes (*Vitis vinifera* L. cv. 'Cardinal'). Our results indicate that this short-term high CO₂ treatment had a residual effect and significantly reduced decay incidence of table grapes during low temperature storage and upon transfer to 20 °C. Our results indicate that during low temperature storage the expression pattern differed between the two tested PR genes. So, while the abundance of *Vcgsn1* transcript increased sharply at the beginning of storage at 0 °C, the increase in *Vcchit1b* mRNA levels was paralleled by the change in total decay. High CO₂ pretreatment restrained the up-regulation of *Vcgsn1* gene expression and delayed the accumulation of *Vcchit1b* transcript as compared with non-treated grapes. Upon transfer to 20 °C after 33 days of cold storage, when attainment of maximum total decay was observed, there was a sharp increase in the accumulation of *Vcchit1b* mRNA in both treated and non-treated grapes, which was higher in the non-treated ones. Our results point out that the expression of class I chitinase and β -1,3-glucanase genes is not enhanced in CO₂-treated grapes which control total fungal decay. These results suggest, then, that the efficacy of high CO₂ pretreatment in reducing total fungal decay is not mediated by induction of the above-mentioned PR genes.

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Keywords: Table grapes; Postharvest technology; Carbon dioxide; *Botrytis cinerea*; Pathogenesis-related proteins; Gene expression

1. Introduction

Postharvest deterioration of table grapes normally results from fungal decay, largely caused by *Botrytis cinerea*, and desiccation of stems and pedicels, which limits prolonged storage of grapes at low temperature. Control against *Botrytis* disease during storage and transportation of grapes is currently achieved by application of fungicides (Luvisi et al., 1992). However, fungicides and chemical treatments may cause damage to grape berries if used excessively, and some

consumers develop allergic reactions. Moreover, frequent prophylactic use of fungicides may lead to multiple resistance in the pathogen population (Raposo et al., 1996; Alfonso et al., 2000). Some alternative strategies have been tried in the place of fungicides (Yahia et al., 1983; Crisosto et al., 2002; Lydakis and Aked, 2003; Retamales et al., 2003). However, to evaluate the efficacy of postharvest treatments for control of decay, we need to know whether these treatments have a direct effect on the fruit's defense responses.

Plant resistance is correlated with the activation of several defense mechanisms including the transcriptional activation of numerous defense-related genes, deposition of mechanical barriers, accumulation of phytoalexins and synthesis of specific pathogenesis-related (PR) proteins. Among PR pro-

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teins, the most fully characterized enzymes are chitinases and β -1,3-glucanases which hydrolyze polymers of fungal cell walls, and it has therefore been suggested that both enzymes are involved in plant defense mechanisms against fungal infection (Boller, 1985; Collinge et al., 1993). Chitinases and β -1,3-glucanases, generally encoded by multigenic families, have been classified by sequence similarity into six and four families, respectively. Also, various studies have demonstrated that transgenic plants overexpressing chitinase and β -1,3-glucanase genes show enhanced resistance to fungal infection (Zhu et al., 1994; Grison et al., 1996).

Multiple isoforms of chitinase and β -1,3-glucanase have been reported in grapes (Busam et al., 1997; Robinson et al., 1997), but the available data concerning their expression in grape berries are limited. Increased levels of chitinases and glucanase mRNAs, or their activities, have been reported in grapevine leaves infected by *Botrytis cinerea* (Derckel et al., 1996; Renault et al., 1996). Busam et al. (1997) reported that the expression of a class III chitinase gene might serve as a marker for systemic acquired resistance in grapevine leaves. In stored tropical fruit, coordinate accumulation of PR proteins such as chitinase-like protein and β -1,3-glucanase has been reported in fruit able to withstand chilling temperature storage (Merodio et al., 1998). However, there are no studies showing changes in the transcript accumulation of defense-related genes in response to high CO₂ levels.

The purpose of this study was to investigate whether the effect of 20% CO₂ on natural postharvest decay control of table grapes directly affects the expression of specific PR genes. The effect of pretreatment with 20% CO₂ on chitinase activity and expression of cDNAs encoding a class I chitinase (*Vcchit1b*) and β -1,3-glucanase (*Vcgns1*) was analyzed. Our results indicate that the tested PR genes are not induced in CO₂-treated grapes that are able to control fungal attack. High CO₂ pretreatment may have an indirect effect on the expression of the class I chitinase gene, and it has a clear effect on avoiding class I β -1,3-glucanase gene induction.

2. Materials and methods

2.1. Plant material

Table grapes (*Vitis vinifera* L. cv. Cardinal) were harvested at random in Camas (Sevilla, Spain) in July. Early-harvest mature berries were used in this work (12.7% total soluble solids; 0.81% tartaric acid). Immediately after harvesting, field-packaged bunches were transported to the laboratory, where fruit were forced-air-cooled for 14 h at -1°C . After cooling, bunches free from physical and pathological defects were randomly divided into two lots and stored at $0 \pm 0.5^{\circ}\text{C}$ and 95% relative humidity (RH) in two sealed neoprene containers of 1 m³ capacity. Ten plastic boxes containing about 3 kg of table grapes per box were stored in each container. One lot was stored under normal atmosphere for 33 days (non-treated fruit) and the other under a gas mixture con-

taining 20% CO₂ + 20% O₂ + 60% N₂ (CO₂-treated fruit) for 3 days. This CO₂ concentration was maintained during the pretreatment experiment and it was measured daily using an automated system gas chromatograph equipped with a thermal conductivity detector and Poraplot Q column (Varian Chrompack CP20033P). After 3 days, CO₂-treated grapes were transferred to air under the same conditions as the non-treated fruit until the end of the storage period. After 12 and 33 days CO₂-treated and non-treated grapes were transferred to ventilated storage containers for 2 days at 20°C and 95% RH, to simulate shelf-life during marketing. Ten clusters were sampled periodically during low temperature storage and at the end of their shelf-life. Berries obtained from five clusters (approximately 300 g each cluster) were peeled and the skin was frozen in liquid nitrogen, ground to a fine powder and stored at -80°C until analysis.

2.2. Evaluation of storage decay

Storage decay was evaluated on the basis of the total decay after removing and weighing the healthy berries. The weight of the decayed berry was calculated by subtracting healthy berries from the total cluster weight. Thus, total decay was expressed as a percentage of decayed berries with respect to the original cluster weight.

2.3. cDNA cloning

Total RNA was isolated from 4 g of frozen berry skin tissues according to Salzman et al. (1999). RT-PCR and 5'-3' RACE were used in cloning the full-length cDNA clones of class I chitinase and β -1,3-glucanase. Partial cDNA clones of class I chitinase and β -1,3-glucanase were obtained by RT-PCR. cDNA synthesis was performed with 10 μg of total RNA from the skin tissues of non-treated and CO₂-treated grapes stored at 0°C . The reaction was carried out in the presence of 500 ng of oligo-dT with 100 units of Reverse Transcriptase (Ecogen). Chitinase and β -1,3-glucanase gene DNA fragments were obtained by PCR amplification using the cDNA as template and degenerate oligonucleotide primers complementary to conserved peptide regions of the class I chitinase and β -1,3-glucanase. A 550-bp fragment of class I chitinase was amplified by combining the sense primer 5'-TGC/T TGC AGC AAG/A TTC/T GGC/T TG/TG/C TG-3', corresponding to the peptide motif CCS(K/Q)FG(F/W)C of the chitin-binding domain, and the antisense primer 5'-A/C/T/GGA C/TTG A/C/T/GGG A/C/T/GGT CAT CCA GAA CCA-3' derived from the peptide WFWMT(A/P)QS. A 850-bp fragment of class I β -1,3-glucanase was amplified using a sense primer 5'-TA/C/T/GG GTG TA/C/T/GT GC/TT ATG GAA TGC T-3' derived from the conserved peptide VGVCYGML, and the antisense primer 5'-CTC A/GTC AAA CAT G/AGC AAA A/T/C/GAG/T/A G/A-3' corresponding to the peptide (L/I)FAMFDE. Both PCR-fragments were cloned into pGEMT (Promega) and confirmed by sequencing. The sequences were used to select

oligonucleotide primers for performing both 5'- and 3'-rapid amplification of cDNA ends (RACE) to obtain the full-length. The 5'/3' RACE kit (Roche) was applied according to the manufacturer's instructions using total RNA isolated to synthesize the cDNA mentioned above. The chitinase and β -1,3-glucanase 5' and 3' PCR-RACE products were subcloned and sequenced. The sequences of these PCR-RACE products and the chitinase 550-bp and β -1,3-glucanase 850-bp internal PCR products yielded overlapping PCR products extending to the 5' and 3' ends of the cDNA.

2.4. Northern-blot hybridization

Samples of denatured total RNA (10 μ g) from the skin were fractionated and blotted as described in Sanchez-Ballesta et al. (2000). Equal loading was confirmed by ethidium bromide staining and by membrane staining with methylene blue. As probes we used the full-length cDNAs *Vcchit1b* and *Vcgns1* random-primer labeled with α^{32} P-dCTP. Filters were prehybridized and hybridized at 65 °C in 7% sodium dodecyl sulfate, 0.33 M phosphate buffer, pH 7.2 and 1 mM EDTA, then washed twice in 2 \times SSC, 0.1% SDS at room temperature and twice in 0.1 \times SSC, 0.1% SDS at 65 °C and exposed to Kodak X-Omat SX film at -80 °C. Autoradiographs were digitally scanned and band densities quantified by 20 image densitometry using Scion Image Software (Scion Corporation, Frederick, MD). The 100% was assigned to the maximum optical density value achieved in each northern and the rest of optical densities were normalized to the maximum value and expressed as percentage of relative accumulation (RA).

2.5. Chitinase extraction and activity

Protein was extracted by homogenizing ground frozen berry skin tissues (250 mg fresh weight) at 4 °C in 5 mL of 100 mM sodium acetate buffer, pH 5.0 and 2% (w/v) polyvinylpyrrolidone. The homogenate was centrifuged at 27,000 \times g for 30 min at 4 °C and the clarified supernatant was recovered. Chitinase activity was assayed using a commercial blue enzyme substrate, CM-chitin-RBV solution (Loewe), based on the precipitability of a non-degraded, highly polymerized substrate when acid is added. Chitinase activity was determined utilizing different dilutions from the crude extract until a linear range of activity versus substrate was established. Enzyme activity was assayed by incubating a standard reaction mixture containing 70 μ L of diluted crude enzyme extract (14 μ L of original crude extract), 200 μ L of aqueous CM-chitin-RBV (2 mg mL⁻¹) and 100 mM sodium acetate buffer, pH 5.0 to yield a final reaction volume of 0.8 mL, for 15 min at 37 °C. The reaction was stopped by adding 200 μ L of 2N HCl and cooling on ice for 10 min. The mixture was then centrifuged at 10,000 \times g for 5 min to precipitate the non-degraded substrate. The supernatant containing degraded polymers was diluted (1:1, v/v) with nanop-

ure water and absorbance was measured at 550 nm against a blank reaction (incubation mixture with HCl-treated crude extract). Specific enzyme activity was defined as "absorbance at 550 nm h⁻¹ mg⁻¹ of protein". Protein concentration was measured by the Bradford (1976) method using a protein-dye reagent (Bio-Rad) and BSA as a standard.

2.6. Statistical analyses

Data from at least three replicates per sample were subjected to analysis of variance (ANOVA) (Stargraphics Program, STSC, Rockville, MD). Multiple variance analysis was employed to determine the significance of the data at $P \leq 0.05$. The results presented here are representative of data from two separate experiments performed in succession.

3. Results

3.1. Isolation and sequence analysis of *Vcchit1b* and *Vcgns1* genes

The full lengths of the *Vcchit1b* (GeneBank Accession no. DQ267094) and *Vcgns1* (GeneBank Accession no. DQ267748) cDNAs were isolated using RT-PCR and 5'-3' RACE strategies. The *Vcchit1b* cDNA consisted of 1133 bp with an open reading frame of 942 bp and encoded a polypeptide of 314 amino acids. The amino acid sequence of VcCHIT1b shared 100% identity with the class I chitinases VCHIT1b (Busam et al., 1997) and VvCHIT1a (Robert et al., 2002), previously isolated from 'Ugni Blanc' and 'Pinot Noir' cultivars, respectively. In addition, sequence domains typical of class I chitinase, such as a putative signal peptide of 20 amino acids followed by a cysteine-rich chitin-binding domain, were found in the N-terminal sequence. A hinge domain of only three amino acid residues separated the cysteine-rich domain from the catalytic domain. Also, the VcCHIT1b protein contained a C-terminal extension of at least seven amino acids, suggesting a vacuolar localization. The mature protein of 286 amino acids presented a calculated pI of 8.44 and a calculated molecular mass of 31.27 kDa.

The full-length cDNA sequence of the *Vcgns1* consisted of 1316 bp and contained an open reading frame of 1080 bp encoding a protein of 360 amino acid residues. The amino acid sequence of VcGNS1 shared 69.1 and 74.5% identity with the basic class I β -1,3-glucanases of *Hevea brasiliensis* and *Nicotiana glauca* (*gns1*) (Chye and Cheung, 1995; Castresana et al., 1990), respectively. Comparison with other β -1,3-glucanases in the databases revealed similarities of only 40–55%. The deduced amino acid sequence of VcGNS1 contains both N- and C-terminal signal peptide sequences of 22 and 21 amino acids, respectively, present in the class I β -1,3-glucanase proteins and required for targeting the protein to the vacuole (Meins et al., 1992). It was assumed that N- and C-terminal processing occurs in a manner similar to that reported for class I β -1,3-glucanase from

tobacco (Shinshi et al., 1988), a mature protein of 317 amino acids with a calculated pI of 9.68 and a molecular mass of 34.6 kDa.

3.2. Effect of high CO₂ levels on total fungal decay during postharvest storage at low temperature

In non-treated grapes, total decay increased progressively during postharvest storage at 0 °C, reaching levels of about 25% after 33 days. The beneficial effect of high CO₂ levels on gray mold incidence was demonstrated since the first diseased berries (1.7% of the total decay) were detected only after 22 days of storage (Fig. 1), while in non-treated fruit the onset of the increase was observed after 12 days. The levels attained at the end of storage (33 days) were significantly lower in CO₂-treated fruit than those observed in non-treated fruit.

3.3. Effect of high CO₂ levels on class I chitinase and β -1,3-glucanase mRNA levels and chitinase activity in table grapes during postharvest storage at low temperature

In the skin of non-treated grapes, low-temperature storage drastically increased levels of the *Vcgsn1* mRNA; these remained stable throughout storage, and a decrease in abundance was observed only after 33 days. However, in CO₂-treated grapes although accumulation of the *Vcgsn1* transcript also increased rapidly at 0 °C, this increase was smaller than in non-treated grapes (Fig. 2A). Storage at 0 °C also induced a slow but progressive accumulation of the *Vcchit1b* transcript in the grape skin, reaching the maximum by day 28 and decreasing slightly thereafter (Fig. 2A). However, the CO₂ treatment delayed accumulation of the class I chitinase mRNA levels, increasing after 22 days and remaining stable until the end of storage (Fig. 2A). With regard to chitinase activity (Fig. 2B), it is interesting to note that although activ-

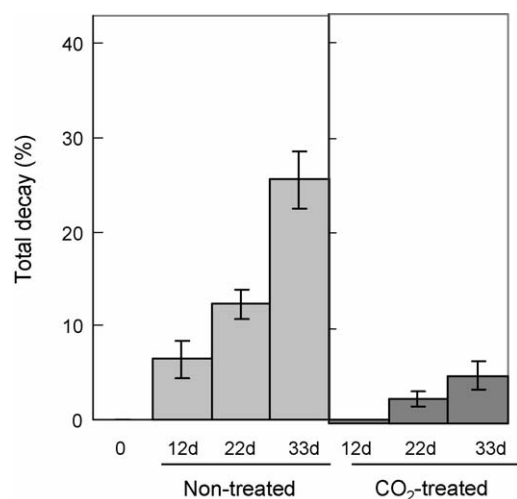


Fig. 1. Total decay (%) in non-treated and CO₂-treated 'Cardinal' table grapes stored at 0 °C for 12, 22 and 33 days. Values are the means of three replicate samples \pm S.E.

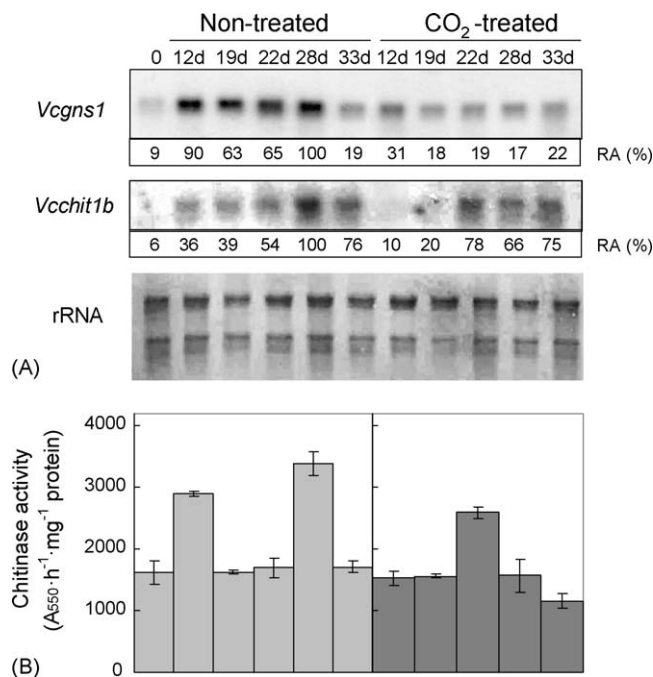


Fig. 2. Effect of high CO₂ levels on *Vcgsn1* and *Vcchit1b* mRNA accumulation in the skin of 'Cardinal' table grapes stored at 0 °C (A). Ten micrograms of total RNA from the skin was fractionated by gel electrophoresis, blotted and hybridized with the *Vcchit1b* and *Vcgsn1* probes. The intensity of the bands was quantified by scanning densitometry of the autoradiographs. Optical densities values were normalized to the maximum value and expressed as percentage of relative accumulation (RA). The equivalence of RNA loading of the lanes was demonstrated by methylene blue staining. (B) Chitinase activity patterns in the skin of non-treated and CO₂-treated 'Cardinal' table grapes during storage at 0 °C. Enzyme activity was expressed as absorbance at 550 nm h⁻¹ mg⁻¹ of protein. Data are averages of two separate experiments ($n=6$) and S.E. are shown by vertical bars.

ity did not increase progressively during storage at 0 °C as occurred with the *Vcchit1b* mRNA levels, the transient peaks in the activity were observed at the time of the increases in accumulation of the transcript (12 and 28 days) (Fig. 2A). By comparison, in CO₂-treated grapes the transient increase in the chitinase activity was observed after 22 days of storage, when an increase in the accumulation of *Vcchit1b* transcript was observed.

3.4. Changes in class I chitinase gene expression, chitinase activity and total decay during the transfer of CO₂-treated and non-treated grapes to 20 °C

After 12 and 33 days of storage at 0 °C, changes in *Vcchit1b* gene expression (Fig. 3A), chitinase activity (Fig. 3B) and total fungal decay (Fig. 3C) in CO₂-treated and non-treated fruit transferred to 20 °C during 2 days, were analyzed. Upon transfer after 12 days of storage, the levels of *Vcchit1b* transcript and chitinase activity in non-treated grapes decreased slightly. In CO₂-treated fruit a slight increase was observed in both *Vcchit1b* gene expression and chitinase activity. The transfer to 20 °C after 33 days of cold storage drastically increased the levels of *Vcchit1b* transcript

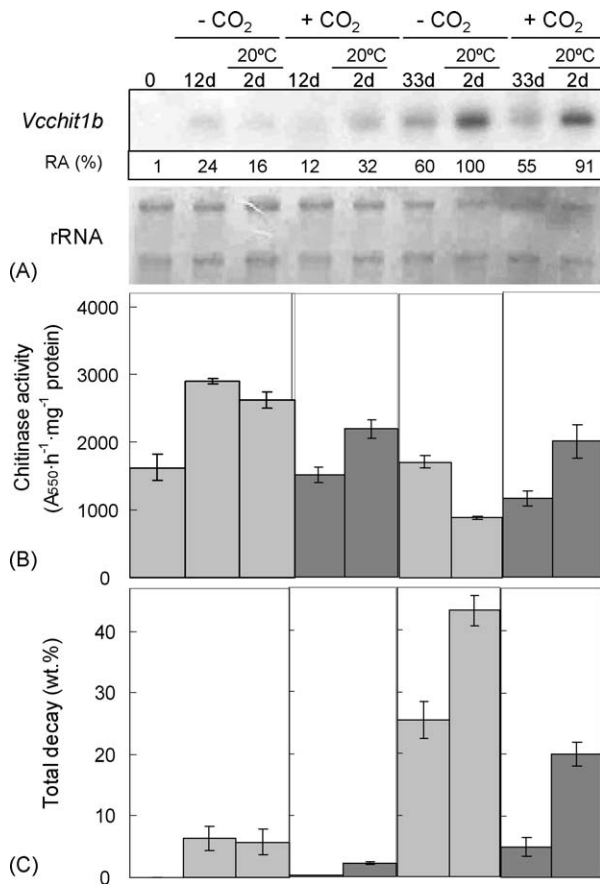


Fig. 3. The pattern of change of mRNA levels (A), chitinase activity (B) and total decay (C) in the skin tissues of non-treated and CO₂-treated 'Cardinal' table grapes stored 12 and 33 days at 0 °C and transferred to 20 °C for 2 days. (A) Ten micrograms of total RNA from the skin was fractionated by gel electrophoresis, blotted and hybridized with the *Vcchit1b* probe. The intensity of the bands was quantified by scanning densitometry of the autoradiographs. Optical densities values were normalized to the maximum value and expressed as percentage of relative accumulation (RA). The equivalence of RNA loading of the lanes was demonstrated by methylene blue staining. (B) Enzyme activity was expressed as absorbance at 550 nm h⁻¹ mg⁻¹ of protein. Data are averages of two separate experiments ($n=6$) and S.E. are shown by vertical bars. (C) Total decay (%) values are the means of three replicate samples \pm S.E.

in skin tissues of both non-treated and CO₂-treated grapes, but this increase was even higher in non-treated ones. This sharp increase in *Vcchit1b* transcript did not correlate with the chitinase activity. However, it was consistent with the total decay increases observed in both series of samples.

4. Discussion

Advances in postharvest handling of table grapes, including the development of treatments for controlling storage decay while avoiding the use of chemicals, have been the focus of interest in recent years (Palou et al., 2002; Chervin et al., 2005). Most of the research has focused on the effectiveness of different postharvest treatments to counteract disease

development in table grapes inoculated with *B. cinerea*. The use of controlled atmosphere (CA) packaging has been proposed as a suitable treatment to replace SO₂ fumigation as a means of controlling grape decay (Yahia et al., 1983; Crisosto et al., 2002; Artés-Hernández et al., 2003). However, in the case of high CO₂ concentrations, applied as a pretreatment for short periods of time, there is little information about its effectiveness in retarding the appearance of symptoms caused by fungal attack and its possible mode of action. Therefore, with a view to assess how effectively high CO₂ concentrations are able to activate specific defense mechanisms against fungal attack, we focused on an analysis of PR gene expression in CO₂-treated and non-treated grapes. Class I chitinase (*Vcchit1b*) and β -1,3-glucanase (*Vcgns1*) cDNAs were isolated from grapes of the 'Cardinal' cultivar of *V. vinifera*. The *Vitis* chitinase and β -1,3-glucanase analyzed here were structurally very similar to the corresponding proteins from *Vitis* or other species. The VcCHIT1b protein is composed of three domains present in the class I chitinase: a Cys rich chitin-binding domain, a Pro rich hinge region and a highly conserved catalytic domain. Moreover, the class I chitinase appeared to be very well preserved in *Vitis*, as the deduced VcCHIT1b protein was identical to the vacuolar class I chitinase from leaves of 'Ugni Blanc' (Robert et al., 2002) and cell cultures of 'Pinot Noir' (Busam et al., 1997). The predicted amino acid sequence of VcGNS1 contains a preserved tryptophan residue, which is implicated in the interaction with the glucan substrate (Ori et al., 1990), and a preserved glutamate, which has been shown to act as a nucleophile in the catalytic mechanism (Varghese et al., 1994). The deduced amino acid sequence of VcGNS1 contains both N- and C-terminal signal peptides, class I β -1,3-glucanases are synthesized as preproteins and the N- and C-terminal extensions are cleaved during or after transport of the protein to the vacuole (Shinshi et al., 1988).

While expression of chitinase and β -1,3-glucanase genes has been extensively studied in plants subjected to specific stress conditions, there is no information in response to high CO₂ levels during postharvest storage applied against fungal infection. Our results indicate that in table grapes cv. Cardinal, the enhanced expression of a cDNA encoding β -1,3-glucanase (*Vcgns1*) (Fig. 2A) observed in non-treated grapes during low temperature storage was constrained by pretreatment with high CO₂ levels, using as a probe the full-length cDNA. Moreover, in these conditions we cannot find any relation between this gene and fungal infection. The marked accumulation of *Vcgns1* mRNA in non-treated grapes at the beginning of storage at 0 °C may indicate that factors other than fungal infection are involved in its induction. In this connection, mRNA accumulation of a class II and class III β -1,3-glucanase from tomato and mandarin, respectively, increased during chilling temperature storage (Ding et al., 2002; Sanchez-Ballesta et al., 2006). Although the effect of low temperature on the expression of β -1,3-glucanase requires further study, high CO₂ levels appears to be a clear effect in avoiding the induction of class I β -1,3-glucanase

genes. The accumulation of *Vcchit1b* transcript (Fig. 2A) during low temperature storage was paralleled by the change in total decay (Fig. 1), using as a probe the full-length cDNA. In this work we observed that total decay increased gradually in non-treated grapes stored at 0 °C. In CO₂-treated grapes, on the other hand, total decay had not increased after 22 days of storage, and class I chitinase gene expression was delayed. With regard to chitinase activity, during low temperature storage the sharp transient increases in total activity matched the increase in *Vcchit1b* transcript levels. Moreover, a differential increase in chitinase activity was observed when the increase in *Vcchit1b* transcript levels was above 30% in both non-treated and CO₂-treated grapes. Upon transfer to 20 °C after 33 days of storage at 0 °C, there was a sharp increase in the accumulation of *Vcchit1b* mRNA in both the treated and non-treated grapes, although it was smaller in the CO₂-treated fruit. With regard to chitinase activity, the transfer to 20 °C at the end of the storage period in non-treated fruit was associated with a decrease in the levels of chitinase activity, although the expression of class I chitinase was sharply enhanced. At this time, chitinase activity in the skin tissues of non-treated grapes decreased significantly, reaching values 45% lower than those quantified in freshly harvested grapes and 55% lower than in CO₂-treated grapes. In CO₂-treated grapes, contrary to what was observed in non-treated grapes, the chitinase activity increased by about 73% with respect to the values prior to transfer. These results are consistent with the change in total decay observed in both series of samples. Effective control against *B. cinerea* and *Penicillium digitatum* has been reported by means of endochitinase combined in mixtures with other antifungal compounds (Ali et al., 2003). During transfer to 20 °C, the lack of correlation between *Vcchit1b* transcript levels and chitinase activity, mostly in non-treated grapes, could be explained in terms of the kinetic and regulatory properties of chitinase enzyme. Many factors, including different post-translational modifications, could be involved in the modulation of chitinase activity. Several isoforms of chitinase have been identified, and it is generally considered that these isoforms represent the products of different members of the chitinase gene family. Additional research is required to study possible mechanisms of regulation of chitinase activity and may provide some useful insights to help restrain fungal infection.

In this work a close link has been established between high CO₂ pretreatment and control of fungal decay. Our results indicate that the expression of class I chitinase and β -1,3-glucanase genes is not enhanced in CO₂-treated grapes that are able to control fungal decay. However, in CO₂-treated grapes, contrary to what was observed in non-treated grapes, there was an upward trend in chitinase activity at the time of maximum growth of fungal decay at 20 °C. We suggest that a mechanism other than induction of the tested PR genes renders grape berries less susceptible to natural postharvest fungal infection. Elsewhere, we reported that the application of 20% CO₂ for short periods of time was effective in reducing the senescence-like responses in peel tissues of fruit

(Escribano et al., 1997) and controlling specific processes associated with low temperature storage (Maldonado et al., 2002). Further analysis is needed to ascertain the mechanism whereby CO₂ treatment can influence the tolerance of table grape to fungal attack before the appearance of the first symptoms and may provide some useful insights to help restrain fungal infection during prolonged low temperature storage.

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ARTÍCULO 6

Molecular characterization of a class I β -1,3-glucanase from *Vitis vinifera* cv. Cardinal.

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***Plant Science* (aceptado)**

RESUMEN

Hemos analizado cómo el almacenamiento a baja temperatura (0°C) y el tratamiento de 3 días con altos niveles de CO₂ (20% CO₂ +20% O₂) afectan la expresión génica de β-1,3-glucanasa de clase I (*Vcgnsl*) y la actividad glucanasa en la uva de mesa roja (*Vitis vinifera* L. cv. Cardinal). Los resultados indican que el almacenamiento a 0°C durante 3 días aumentó los niveles de mRNA de *Vcgnsl* y la actividad β-1,3-glucanasa en la piel de uvas no tratadas. Sin embargo, la acumulación de los transcritos y el nivel de la actividad glucanasa fueron menores en la piel de uvas tratadas con CO₂ durante 3 días, así como cuando la fruta tratada fue transferida a aire. Utilizando la expresión heteróloga del cDNA de *Vcgnsl* en *Escherichia coli*, vimos que codificaba un proteína con actividad glucanasa con un pH óptimo de 6 y temperatura óptima de 45 °C, así como una alta estabilidad a 0°C. Además, la proteína purificada VcGNS1 exhibió actividad crioprotectora *in vitro* para la enzima lábil a congelación L-lactato deshidrogenasa (LDH). Por el contrario, cuando fue medida la actividad de histéresis térmica (THA) de la proteína recombinante VcGNS1, usando calorimetría diferencial de barrido (DSC), los resultados indicaron que no presentó actividad anticongelante. La alta estabilidad de la proteína recombinante a 0°C, y su actividad crioprotectora mostrada en este trabajo, sugiere que VcGNS1 podría participar en la respuesta de la uva de mesa para combatir las condiciones de bajas temperaturas.

**MOLECULAR CHARACTERIZATION OF A CLASS I BETA-1,3-GLUCANASE
FROM *Vitis vinifera* cv. Cardinal**

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Abstract

We have analyzed how low temperature storage (0 °C) and a 3-day treatment of high CO₂ levels (20% CO₂ plus 20% O₂) affect class I β-1,3-glucanase (*Vcgnsl*) gene expression and glucanase activity in the red table grape (*Vitis vinifera* L. cv. Cardinal). The results indicate that storage at 0 °C for 3 days increased *Vcgnsl* mRNA levels and β-1,3-glucanase activity in the skin of non-treated grapes. However, the accumulation of the transcripts, and the level of glucanase activity, were lower in the skin of grapes after 3 days of CO₂ treatment, as well as when treated fruit were transferred to air. By using heterologous expression of the *Vcgnsl* cDNA in *Escherichia coli*, we showed that it encoded a protein with glucanase activity with an optimum pH and temperature of 6 and 45 °C, respectively, and a high stability at 0 °C. Furthermore, the purified VcGNS1 exhibited *in vitro* cryoprotective activity for the freeze labile L-lactate dehydrogenase (LDH) enzyme. In contrast, when the thermal hysteresis activity (THA) of the recombinant VcGNS1 was measured, using differential scanning calorimetry (DSC), the results indicated that it did not show antifreeze activity. The high stability of the recombinant protein at 0 °C, and its cryoprotective activity shown in this work suggest that VcGNS1 may participate in the response of table grape to combat low temperature conditions.

Keywords: Table grapes; Carbon dioxide; Beta-1,3-glucanase; Gene Expression; Cryoprotective; Antifreeze

1. Introduction

Low temperature storage has always been used as the main method to extend the postharvest life of fruit and vegetables. Table grapes are not susceptible to injury at low (not freezing) temperatures, but their storage life is limited due to their high sensitivity to fungal attack. A number of studies have shown that exposure of plants to a moderate temperature stress not only induces resistance to severe stress of this kind, but can also improve tolerance to other stresses [1,2]. In previous studies we have observed that high CO₂ levels applied at low temperature during 3 days reduced total decay in table grapes, thereby maintaining fruit quality [3,4]. The responses of fruit to high CO₂ levels vary considerably among cultivars, and also depend on other environmental conditions of storage. Non-treated grapes responded to temperature shifts in the first stage of storage at 0 °C, activating defense responses related to the phenylpropanoid pathway, whereas the application of high CO₂ levels reduced these responses [5].

In recent years, different studies have identified genes and metabolic pathways involved in the perception and signal transduction of plant responses to extreme temperatures (reviewed by [6]). Certain conserved mechanisms may still operate between chilling-sensitive and chilling-tolerant plants, and even between freezing and chilling tolerance [7]; but it is important to note that most of the studies were conducted in *Arabidopsis thaliana* during cold-acclimation to freezing, and little is known about the molecular basis of cold responses in agronomical important plants. Several studies have led to the identification of cold-responsive genes, many of which encode apoplastic antifreeze proteins (AFPs), late embryogenesis abundant proteins or pathogenesis related proteins (PRs), such as β -1,3-glucanases and chitinases [8].

β -1,3-glucanases (EC 3.2.1.39) hydrolyze the β -1,3-linked glucans found in the cell walls of higher plants, as well as in many fungi [9,10]. Glucanase gene expression may not only be modulated in response to many physiological processes in healthy plants [11,12,13], but also in response to biotic and abiotic stresses [12]. In winter rye, Hon et al. [14] observed that a cold-induced PR protein showed β -1,3-glucanase and cryoprotective activity. Likewise, a class I β -1,3-glucanase purified from tobacco protected thylakoids *in vitro*, isolated from spinach, against freeze-thaw damage [15].

Although isolation of β -1,3-glucanase genes have been reported in grapes [3,16,17], only limited information is presently available on the regulation of gene expression and the function of these proteins. The participation of β -1,3-glucanase in the defense of grapevine leaves against *Botrytis cinerea* has been shown [18,19]. However, in red table grapes we have observed that the efficacy of high CO₂ pretreatment in reducing total fungal decay is not mediated by the induction of class I β -1,3-glucanase and chitinase genes [3], indicating that factors other than fungal infection are involved in the induction of these genes in table grapes.

The aim of the present work was to analyze gene expression of *Vcgns1*, a class I β -1,3-glucanase, in red table grapes as a marker for changes in response to low temperature, and also to assess how high CO₂ levels (20%) modulated its transcript accumulation at 0 °C. As a part of our study to investigate the possible physiological role of class I β -1,3-glucanase in table grapes as a cryoprotectant, and/or an antifreeze, we also report on recombinant expression of *Vcgns1*.

2. Material and Methods

2.1. Plant Material

Table grapes (*Vitis vinifera* L. cv. 'Cardinal') were harvested at random in Camas
5 (Sevilla, Spain) in July. After harvesting, the field-packaged bunches were transported to
the laboratory where fruit were immediately forced-air precooled for 14 hours at -1°C .
After cooling, bunches free from physical and pathological defects were randomly divided
into two lots and stored at $0 \pm 0.5^{\circ}\text{C}$ and 95% relative humidity in two sealed neoprene
containers of 1 m^3 capacity. One lot was stored under a normal atmosphere for 6 days (non-
10 treated fruit), and the other under a gas mixture containing 20% CO_2 + 20% O_2 + 60% N_2
(CO_2 -treated fruit) for 3 days. The grapes were then transferred to air under the same
conditions as non-treated fruit until the end of the storage period.

Ten clusters were sampled periodically, and berries from five clusters (approx. 300
g each cluster) were peeled, and the skin and pulp were frozen in liquid nitrogen, ground to
15 a fine powder, and stored at -80°C until analysis.

2.2. RNA gel blot hybridization

Total RNA was extracted from the skin of grapes according to the method of
Salzman et al. [20]. Samples of denatured total RNA ($10\text{ }\mu\text{g}$) from the skins were
20 fractionated and blotted, as described in Romero et al. [3]. Equal loading was confirmed by
membrane staining with methylene blue. The *Vcgnsl* DNA probe was a random primer
labeled with $\alpha^{32}\text{P}$ -dCTP. Filters were prehybridized and hybridized at 65°C in 7% sodium
dodecyl sulfate, 0.33 M phosphate buffer, pH 7.2, and 1 mM EDTA, then washed twice in

2 x SSC, 0.1% SDS at room temperature and twice in 0.1 x SSC, 0.1% SDS at 65 °C, and exposed to Kodak X-Omat SX film at –80 °C.

2.3. Production of the recombinant VcGNS1 protein in *Escherichia coli*

5 The cDNA fragment of VcGNS1 (GenBank accession number DQ267748) without the N-signal peptide and C-terminal extension was amplified using the forward primer (5'-ATT ATC CTC GAG GTG GGT GTA TGC TAT GGA ATG-3') and the reverse primer (5'-GGC GAA TTC AAA GTT GAT AGA GTA CTT CGG -3') containing *XhoI* and *EcoRI* restriction sites, respectively. The PCR conditions were 30 cycles of 40 s at 95 °C, 10 40 s at 49 °C and 40 s at 72 °C. The amplified DNA fragments were digested with *XhoI* and *EcoRI* and ligated into the multicloning site of the pTrcHisA plasmid (Invitrogen, Carlstad, USA) previously digested with the same enzymes. The vector pTrcHisA-VcGNS1 was transformed into cells of *E. coli* strain TOP10, which were grown at 37 °C in LB-medium with 50 µg mL⁻¹ ampicillin and 0.8 mM glucose until the optical density at 600 nm reached 15 0.6, and then induced with 1 mM isopropyl-β-D-thiogalactoside (IPTG). After 4 h of induction at 37 °C the cells were harvested by centrifugation at 1760g for 20 min at 4 °C and then frozen. Cells were re-suspended in lysis buffer (50 mM sodium phosphate monobasic, 500 mM sodium chloride, 10 mM imidazole, pH 8.0) and DNaseI RNase-Free (Roche); and then disrupted with 1 g of glass beads (150-252 µm, Sigma) in a FastPrep 20 machine (FP120, Bio101, Savant). The cell extract was centrifuged at 1580g for 10 min at 4 °C. The soluble recombinant His-tag VcGNS1 protein was incubated with Ni-NTA agarose resin (QIAexpress, Qiagen, Germany) for 1 h at 4 °C with shaking, before the extract-resin mixture was loaded into a column. Contaminating proteins were eluted by washing the column with 8 mL of buffer (50 mM sodium phosphate monobasic, 500 mM sodium

chloride, 40 mM imidazole, pH 8.0). Bound VcGNS1 was eluted from the Ni-NTA column with elution buffer (5 x 1 mL 50 mM sodium phosphate monobasic, 500 mM sodium chloride, 300 mM imidazole, pH 8.0). The purified fusion protein was concentrated with buffer exchange into 50 mM Tris-HCl, pH 7.4 for enzymatic assays, into 20 mM sodium acetate buffer pH 5.0 for *in vitro* antifungal assays or doubled distilled water for *in vitro* cryoprotective and antifreeze assays by ultrafiltration on ultrafree biomax-5K (Millipore), and then stored at -20 °C. Protein concentration was determined according to the Bradford method [21] using a protein-dye reagent (Bio-Rad) and bovine serum albumin as a standard.

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2.4. Gel electrophoresis and protein blot analyses

Protein analysis was performed on 12% sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE) according to Laemmli [22], using Mini-Protean II Cell (Bio-Rad) equipment. Protein samples were prepared by boiling for 10 min in 2X SDS loading buffer (62.5 mM Tris-HCl, pH 6.8, 2% SDS, 20% glycerol, and 0.05 % bromophenol blue). For reducing conditions, samples were mixed with an equal volume of loading buffer supplemented previously with 10% β -mercaptoethanol. Protein bands were visualized by staining with Coomassie brilliant blue R-250. The molecular mass of the separated polypeptides was estimated by comparison with the mobility of pre-stained standard low molecular mass range proteins (Bio-Rad).

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After standard PAGE was performed proteins were electro-transferred to PVDF membranes (Amersham) with a Mini Trans-Blot Cell (Bio-Rad). The Western blot was probed with a 1:5000 dilution of polyclonal anti-PR2 sera from tobacco, kindly provided by

Dr Fritig (Strasbourg, France), which were detected with a 1:5000 dilution of rabbit antiserum against IgG horseradish peroxidase conjugate (Amersham). The immuno-complexes were visualized using the enhanced chemiluminescence (ECL[®]) detection system (Amersham).

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2.5. Protein extracts preparation

Ground frozen berry skin tissue (3 g FW) was homogenized in 10 mL of 100 mM sodium acetate buffer, pH 5.0, and 2% (w/v) polyvinylpyrrolidone. The homogenate was centrifuged at 35000g for 30 min. After removal of precipitated material the supernatant
10 was adjusted to 95% saturation with ammonium sulphate, and centrifuged at 20000g for 20 min. The precipitate was re-suspended in 100 mM sodium acetate buffer, pH 5.0. All steps were carried out at 4 °C.

2.6. β -1,3-glucanase activity assay

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2.6.1. Protein extracts

β -1,3-glucanase activity was quantified measuring the reducing sugar released from the substrate *Laminaria digitata* laminarin (Sigma). 50 μ L of extract was added to 300 μ L of substrate (0.5 mg) in 100 mM sodium acetate buffer, pH 5.0. The reaction was stopped
20 with 35 μ L of NaOH after 8 h of incubation at 37 °C and cooling on ice for 10 min. The reducing sugar was determined according to Dygert et al. [23]. D-glucose at concentrations from 2.5 to 120 μ g mL⁻¹ in buffer was used as a standard. Enzyme activity was defined as nmol glucose equivalents h⁻¹ g FW⁻¹. Assays were determined in three replicated samples from three independent extractions.

2.6.2. Recombinant VcGNS1 protein

Optimum temperature value was determined by measuring the specific activity of 1 µg of purified VcGNS1 with 2 mg of *L. digitata* laminarin (Sigma) in 100 mM sodium acetate buffer, pH 6.0, at temperatures ranging between 0 °C and 75 °C. Optimum pH value was determined at 45 °C by running the enzymatic assay with 1 µg of purified VcGNS1 in 2 mg of *L. digitata* laminarin (Sigma) in 100 mM phosphoric acid (pH 2.0), sodium acetate (pH 4.0-6.0), sodium phosphate dibasic (pH 7.0), Tris-HCl (pH 9.0) and sodium phosphate monobasic (pH 12) buffers. The mixtures were incubated with shaking for 60 min and the reducing sugars were measured as described above. The activity of VcGNS1 was recorded as the release of µmoles glucose equivalents min⁻¹ mg protein⁻¹. Assays were determined in three replicated samples from three independent purifications of VcGNS1.

To determine the thermal and pH stability of the recombinant VcGNS1 the purified protein (1 µg) was incubated in 100 mM sodium acetate buffer, pH 6.0, without laminarin, for 1 h at temperatures between 0 °C and 75 °C and in the buffer at different pHs at 45 °C, respectively. Subsequently, the residual activity was measured with 2 mg of laminarin as described above. Assays were determined in three replicated samples from three independent purifications of VcGNS1.

2.7. Kinetic parameters

The Michaelis-Menten constants K_m and k_{cat} were determined from the Hanes-Wolf representation of data obtained by measuring the initial rate of substrate hydrolysis. 1 µg of purified VcGNS1 was incubated at 45 °C with increasing concentrations of laminarin (0-5 mg mL⁻¹) in 100 mM sodium acetate buffer, pH 6.0. After the reaction was stopped the

liberated glucose was measured as described above. The activation energy (E_a) was calculated by the method of Segel et al. [24], using the linear form of Arrhenius equation:

$$\log k = \frac{-E_a}{2.3R} \frac{1}{T} + \log A$$

in which R is the molar gas constant, T is the absolute temperature and k the specific
5 reaction rate constant. For enzyme-catalyzed reactions $\log V_{max}$ can be plotted instead of $\log k$.

The effect of δ -gluconolactone (Sigma) on the activity of the purified enzyme was measured as described previously Notario et al. [25].

10 2.8. Assay for cryoprotective activity

The *in vitro* cryoprotective activity was determined following the method described by Lin and Thomashow [26], with slight modifications. Lactate dehydrogenase (LDH, EC 1.1.1.23, Type V-S from rabbit muscle, Sigma, St. Louis, MO, USA) was diluted to 87.6 $\mu\text{g mL}^{-1}$ in 20 mM potassium phosphate buffer, pH 7.5, and used as a freeze-labile stock
15 enzyme solution. Samples, either VcGNS1 protein fractions or bovine serum albumin (BSA, Sigma, St. Louis, MO, USA), were diluted to varying concentrations and mixed with 2.364 μg of LDH from the stock solution. The resulting solution (300 μL) was frozen in liquid nitrogen for 30 s and then thawed at room temperature for 5 min. The freeze-thaw process was carried out three times and the residual LDH activity was then measured. LDH
20 enzymatic activity was determined in aliquots of 30 μL of the mixtures in a final volume of 1.5 mL of the reaction assay buffer (80 mM Tris-HCl pH 7.5, 100 mM KCl, 2 mM pyruvate and 30 mM NADH), at room temperature. NAD^+ production was monitored as the

decrease of absorbance at 340 nm for 4 min. The data are showed as the percentage of the activity present in unfrozen controls. Assays were determined in three replicated samples.

2.9. Antifreeze activity measurement

5 The differential scanning calorimetry (DSC) was used to determine the antifreeze activity by measuring the thermal hysteresis activity (THA). DSC analysis was conducted using a differential scanning calorimeter (DSC822e, Mettler-Toledo Inc., Columbus, OH, USA) equipped with a liquid nitrogen cooling accessory. The instrument was calibrated using Indium and n-octane, and an empty aluminum pan was used as reference. An
10 antifreeze protein (type III) from antarctic fish, kindly provided by Dr. De Vries (Illinois, USA), and BSA (AFP-free solution) were used as standards in order to make a comparison between solutions with and without antifreeze activity. Recombinant VcGNS1 protein (5 mg·mL⁻¹) dissolved in double distilled water and 3-4 µl sample was weighed into 40 µL Mettler-Toledo coated aluminum pans. Pans with samples were immediately hermetically
15 sealed and cooled from 25 °C to -40 °C at 10 °C min⁻¹, frozen at this temperature for 5 min, and heated to melt (10 °C min⁻¹). The samples were cooled at -30°C (10 °C min⁻¹) for 5 min, and warmed up slowly to various partial-melt temperatures (0.5 °C min⁻¹). To allow ice-protein interaction, samples were held at this temperature (T_h, hold temperature) for 10 min before being re-cooled at the same rate of 0.5 °C min⁻¹ to -25 °C, during which the onset
20 temperature of crystallization (T_c) was recorded using STARe software (Mettler-Toledo). THA was defined as the difference between T_h and T_c, THA=T_h – T_c.

2.10. Statistical analysis

The data from at least three replicates per sample were subjected to analysis of variance (One-way ANOVA) using the LHD test to determine the level of significance at $P \leq 0.05$ (Statgraphics Plus version 5.1, STSC, Rockville, Md.).

5 **3. Results**

3.1. Effect of low temperature and high CO₂ on Vcgnsl mRNA levels and β -1,3-glucanase activity

In the skin of non-treated grapes low temperature sharply increased the levels of the transcript after 3 and 6 days of storage (Fig. 1A). In contrast, high CO₂ levels applied during 3 days at 0 °C decreased the accumulation of the *Vcgnsl* mRNA, but levels increased slightly when treated grapes were transferred to air for 3 days, although the levels were always lower than in the non-treated. Glucanase activity increased significantly after 3 days at 0 °C in non-treated grapes, and then decreased after 6 days (Fig. 1B). The increase of glucanase activity after 3 days of CO₂ at 0 °C treatment was lower than in non-treated grapes, increasing slightly thereafter.

3.2. Expression and purification of VcGNS1

The full-length of the VcGNS1 was previously isolated from the skin of table grape using RT-PCR and 5'-3' RACE strategies [3]. The predicted amino acids of VcGNS1 cDNA shared homology with basic class I β -1,3-glucanases containing a N-terminal signal peptide cleavage site located between residues 22 (Lys) and 23 (Ser), and a C-terminal

extension of 23 amino acids with a *N*-glycosylation site, and required for targeting the protein to the vacuole [27,28].

To determine whether the VcGNS1 cDNA encoded a protein with glucanase activity, and to perform *in vitro* cryoprotective and antifreeze assays, the cDNA fragment corresponding to the mature protein (without the putative N-terminal transit peptide and the C-terminal extension, amino acid residues 23 to 338) was expressed in TOP10 *E. coli* cells as a pTrcHisA-VcGNS1 fusion protein. The VcGNS1 protein was induced in the presence of 1 mM IPTG at 37 °C for 4 h and purified with a Ni-NTA affinity column. After purification, gel electrophoresis of both reduced and unreduced VcGNS1 yielded a single band of 43 and 40 kDa respectively (Fig. 2A), suggesting that the native protein occurs as a monomer. Western blot analysis with an antiserum against tobacco PR2 showed a positive band with the same molecular mass (Fig. 2B).

3.3. Effects of temperature and pH on enzyme activity and stability

The enzymatic activity of the recombinant β -1,3-glucanase was measured over a pH (2-12) and temperature (0-70 °C) range by assaying the production of reduced sugars from laminarin (Fig. 3). The pH optimum for recombinant VcGNS1 was 6, decreasing sharply at pH values above 6.5 or below 5.5. The temperature optimum was 45 °C, but the recombinant VcGNS1 retained some hydrolytic activity at different temperatures assayed. In terms of stability, the recombinant protein was able to catalyze the hydrolysis of laminarin over a wide range of pH, 2 to 9, and temperature, 0 °C to 45 °C, being inactive at pH 12 and at temperatures higher than 60 °C. Interestingly, the recombinant protein showed

the optimum stability at 0 °C, reaching values significantly higher to those achieved when the activity was measured at 45 °C.

3.4. Kinetic properties

5 The recombinant β -1,3-glucanase obeys Michaelis-Menten kinetic. A linear curve was obtained from the Hanes-Wolf plot for the hydrolysis of laminarin at concentrations of 0-5 mg/mL, yielding an apparent K_m value of 0.78 mg/mL which, corresponds to 0.195 mM. The catalytic rate constant, k_{cat} , is 7.96 s^{-1} and the specificity or catalytic efficiency factor, k_{cat}/K_m , $40.82 \text{ s}^{-1} \text{ mM}^{-1}$. The calculated E_a was 19.95 kJ/mol for laminarin hydrolysis
10 (Table 1). Moreover, the VcGNS1 did not show inhibition with δ -gluconolactone (1 to 20 mM), a potent inhibitor of exo- β -glucanases at low concentrations (Notario et al, 1976), indicating an endotype mode of action for the recombinant enzyme (data not shown).

3.5. Cryoprotective activity of recombinant VcGNS1

15 The ability of recombinant β -1,3-glucanase to preserve LDH activity following freeze-thaw cycles was compared with the level of cryoprotection provided by BSA. The cryoprotective activity of recombinant VcGNS1 and BSA was then assessed by determining whether they could protect LDH against freeze inactivation. Without the addition of a cryoprotectant three freeze-thaw cycles resulted in a reduction of more that
20 80% in LDH activity (Fig. 4). The addition of VcGNS1 or BSA in protein:enzyme molar ratios from 1 to 4 significantly protected LDH activity. Recombinant VcGNS1 was shown to be less efficient than BSA in protecting LDH at molar ratios from 1 to 3. At a molar ratio of 4, VcGNS1 was as efficient as BSA in protecting LDH activity against freeze

inactivation, maintaining around 70% of initial LDH activity. On the contrary, the addition of sucrose at similar concentrations failed to protect LDH under identical freeze-thawing conditions.

5 3.6. Thermal hysteresis activity of recombinant VcGNS1

DSC curves of the recrystallization of different partially melted protein-water systems are presented in Fig. 5. A delay of 0.4 °C in the onset temperature of refreezing was observed in a partially melted AFP system. In recombinant VcGNS1 solution, recrystallization of the melted part started immediately after the temperature dropped, and
10 the exothermic peak appeared without delay. This indicated that the VcGNS1, like AFP-free BSA solution, had no thermal hysteresis effect.

4. Discussion

Grapes are classified as a chilling tolerant fruit, and are normally injured at
15 temperatures below -20 °C. Previous results indicated that table grapes cv. Cardinal could be sensitive to temperature shifts at 0 °C, and that high CO₂ levels applied as a pretreatment could regulate these responses [4]. To further identify the mechanisms associated with the response of table grapes at 0 °C, and to determine whether high CO₂ levels could modulate them, we have analyzed changes in β -1,3-glucanase gene expression in the first stage of
20 storage. There have been several previous reports of PR proteins induced by low temperature. In winter rye, one of the PR proteins induced in response to low temperature showed β -1,3-glucanase and cryoprotective activity [14]. In citrus, Sanchez-Ballesta et al. [29] observed that changes in gene expression of a class III β -1,3-glucanase were linked to postharvest chilling-induced cell damage. In tomato exposed at chilling temperature a class

II β -1,3-glucanase mRNA was induced [30]. In previous work, we have isolated a class I β -1,3-glucanase (*VcgnsI*) cDNA from the skin of table grape [3]. The levels of the *VcgnsI* transcript increased in non-treated grapes after 12 days at 0 °C, but we did not find any relation between *VcgnsI* gene expression and fungal attack, indicating that factors other than fungal infection are involved in *VcgnsI* gene expression in table grapes. In this work we observed that low temperature by itself has a clear effect on *VcgnsI* gene expression and glucanase activity. Thus, after 3 days at 0 °C a sharp increase in the level of *VcgnsI* mRNA was observed in the skin of non-treated grapes, maintaining the level after 6 days. In contrast, 3 days CO₂-treatment reduced the accumulation of the transcript observed at 0 °C, with a slight increase in the levels when treated grapes were transferred to air (Fig. 1A). Likewise, although glucanase activity increased in response to low temperature, the increase was higher after 3 days at 0 °C in the non-treated grapes. Previously, similar results were observed in non-treated grapes, where phenylpropanoid gene expression, total anthocyanin accumulation and antioxidant activity were activated during the first stage of storage at 0 °C, whereas the application of high CO₂ treatment reduced these responses [4]. These results reinforce the idea that high CO₂ levels applied at 0 °C as a pretreatment of 3 days can modulate the responses induced in non-treated grapes in the first stage of storage at 0 °C.

To determine whether the *VcgnsI* cDNA isolated from table grape encoded a protein with glucanase activity, and to analyze its functionality, the protein was produced by the pTrcHis expression system in *E. coli*. The purified recombinant protein showed a single protein band in SDS-PAGE. The molecular mass of the recombinant VcGNS1 was 40 kDa, and this value agreed with the molecular mass calculated from the deduced polypeptide. The purified VcGNS1 showed β -1,3-glucanase activity for laminarin

hydrolysis with a pH optimum higher than other plant β -1,3-glucanase enzymes [31,32], but with similar optimum temperature. The VcGNS1 protein was relatively more thermostable than the β -1,3-glucanases from *Boscia senegalensis* [32] and barley [33], being active over a wide range of temperatures. The recombinant glucanase displayed 27% of relative activity at 0 °C and, interestingly at this temperature, VcGNS1 showed a higher thermostability after 1 h without substrate. The E_a for VcGNS1 is lower than values obtained for other carbohydrate hydrolases [32] and constant over the studied temperature range, indicating that the enzyme does not undergo major structural changes within this range. In winter rye glucanases presented the maximal activity at temperatures around 30 °C, and there was clear evidence of activity at zero and subzero temperatures [34]. However, to our knowledge, this is the first report where a β -1,3-glucanase from fruit showed low values of E_a and hydrolytic activity at cold temperatures. Kinetics analyses of the recombinant VcGNS1 during hydrolysis of laminarin allowed the calculation of a K_m value (0.195 μ M) which is substantially higher than that reported for β -1,3-glucanases from other plants [32,35]. However, the turnover number (k_{cat} 7.96 s⁻¹) was significantly lower than values reported for plant glucanases [33,35]. Furthermore, VcGNS1 could behave as an endo-splitting hydrolase because of the non inhibitory effect of δ -gluconolactone on the enzymatic activity observed in this work (data not shown). In this respect, this enzyme is comparable to other plant β -1,3-glucanases isolated [32,33,36,37].

It has been reported that proteins identified as PRs that accumulate in winter cereals during cold acclimation function as antifreeze proteins, by inhibiting extracellular ice growth under freezing temperatures [14]. Yaish et al. [34] support the hypothesis that recombinant winter rye glucanases have evolved to inhibit the formation of large ice

crystals, in addition to the capacity to degrade glucans at low temperature. In contrast, the recombinant VcGNS1 did not show antifreeze activity when the THA was determined by DSC. In spinach and cabbage leaves β -1,3-glucanase proteins were accumulated during cold acclimation, and glucanase of class I had potent cryoprotective activity [15]. Likewise, a PR-5 protein from groundnut showed *in vitro* cryoprotective activity against LDH [38]. However, this appears not to be a general effect of stress-induced PR proteins. A tobacco class I chitinase did not demonstrate any cryoprotective effects [15]. In chilling-sensitive mandarins the recombinant class III β -1,3-glucanase protein, likewise, showed glucanase but not cryoprotective activity [29]. In this study we demonstrate that VcGNS1 had cryoprotection activity. Assay for freeze-thawing enzyme inactivation was done with LDH, because of its sensitivity to different stresses. A comparison of the cryoprotection conferred by VcGNS1 revealed that it was similar to that of BSA, which is a known cryoprotectant [39]. Similar results have been observed with WAP18, a PR10 from mulberry [40]; COR15am, a LEA-like protein from *Arabidopsis* [41]; and winter rye apoplastic proteins [42], which in all situations exhibited a similar value to BSA. In contrast the cryoprotective activities of COR85 and PCA60, cold-induced dehydrins, were found to be around four or two-fold higher than that for BSA [43,44]; but CrCOR15, a dehydrin from citrus fruit revealed a cryoprotective activity similar to BSA [45]. The percentage of polar residues in VcGNS1 is around 40% as occur in a PR-10 protein such as WAP18 [40]. These authors indicated that the lower-cryoprotective activity of WAP18, in comparison with other cryoprotectants, may be partially related to the lower-ratio of polar residues in the surface of the protein.

In conclusion, we have identified a class I β -1,3-glucanase from table grapes that displays glucanase activity as well as *in vitro* cryoprotective but not antifreeze activity.

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Figure Captions

Fig. 1. Effect of low temperature and high CO₂ pretreatment on *Vcgnsl* mRNA accumulation (A) and β -1,3-glucanase activity (B) in the skin of 'Cardinal' table grapes (A) 10 μ g of total RNA from the skin was fractionated by gel electrophoresis, blotted and hybridized with the *Vcgnsl* probe. The equivalence of RNA loading of the lanes was demonstrated by methylene blue staining. (B) Time courses of β -1,3-glucanase activity in the skin of non-treated and CO₂-treated 'Cardinal' table grapes stored at 0 °C. Error bars represent S.E (n=9). Values labeled with the same letter are not different at the 5% significance level.

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Fig. 2. (A) Recombinant VcGNS1 protein was analysed by SDS-PAGE (12% polyacrylamide) and stained by Coomassie blue. Lanes 2 and 3 were loaded with 2 μ g of reduced (with 10 % β -mercaptoethanol) and unreduced protein. Lane 1 was loaded with low molecular mass reference proteins and sizes are indicated on the left. (B) Immunoblot of a similar gel with unreduced VcGNS1. The blot was incubated with polyclonal anti-PR2 sera from tobacco.

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Fig. 3. Effect of pH and temperature on the activity (—●—) and stability (—○—) of recombinant VcGNS1. Optimum temperature was determined by measuring the specific activity of 1 μ g of purified VcGNS1 in a range of temperatures from 0 °C to 80 °C at pH 6.0. Optimum pH was determined by measuring the activity at 45 °C in the range of pH 2 to 12. Stability was assessed by measuring the residual activity after 1 h of incubation at different pH and temperatures. For all experiments, laminarin degradation was measured

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under standard assay conditions. Values presented are expressed in relative activity (percent of the greatest activity detected). Error bars represent S.E (n=9).

Fig. 4. Cryoprotection of LDH by recombinant VcGNS1. A LDH solution was frozen with different concentrations of VcGNS1, BSA or sucrose. The samples were thawed at room temperature and the LDH activity was measured. The relative activity represents the amount of LDH activity remaining after a freeze-thaw treatment as a percentage of the control enzyme activity. Error bars represent S.E (n=3).

Fig. 5. Refreezing DSC curves ($0.5\text{ }^{\circ}\text{C min}^{-1}$) of partially melted protein-water systems. A) AFP-III B) BSA C) recombinant VcGNS1.

Figure(s)

Figure 1

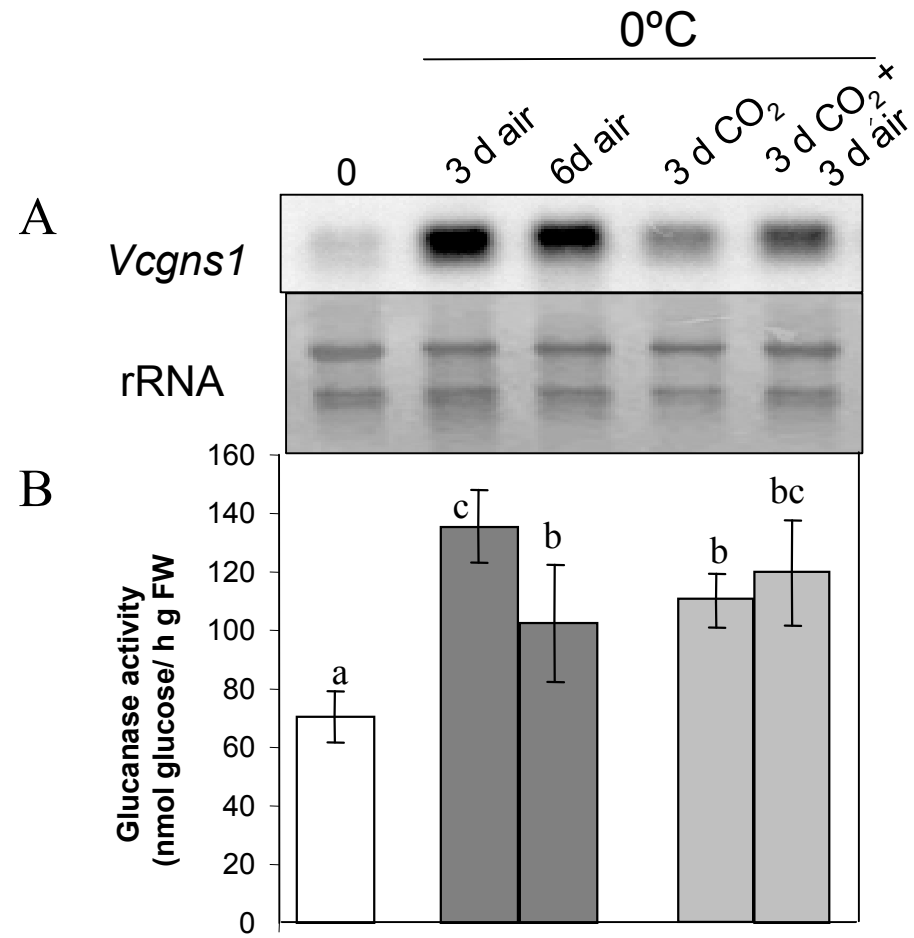


Figure 2

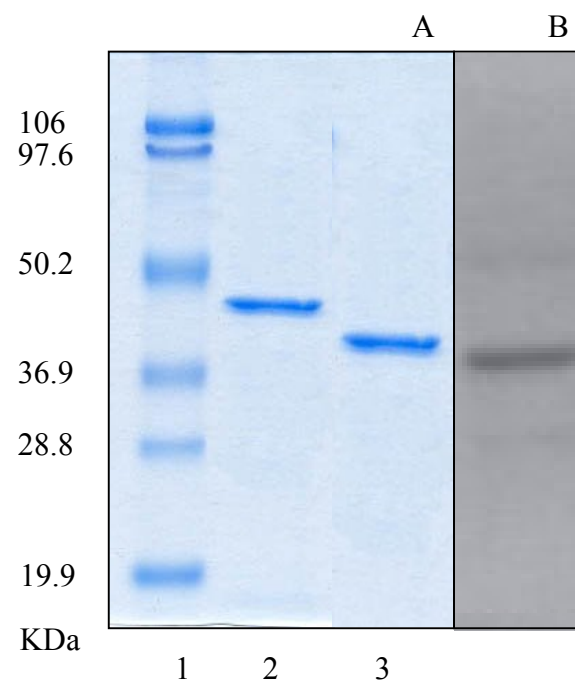


Figure 3

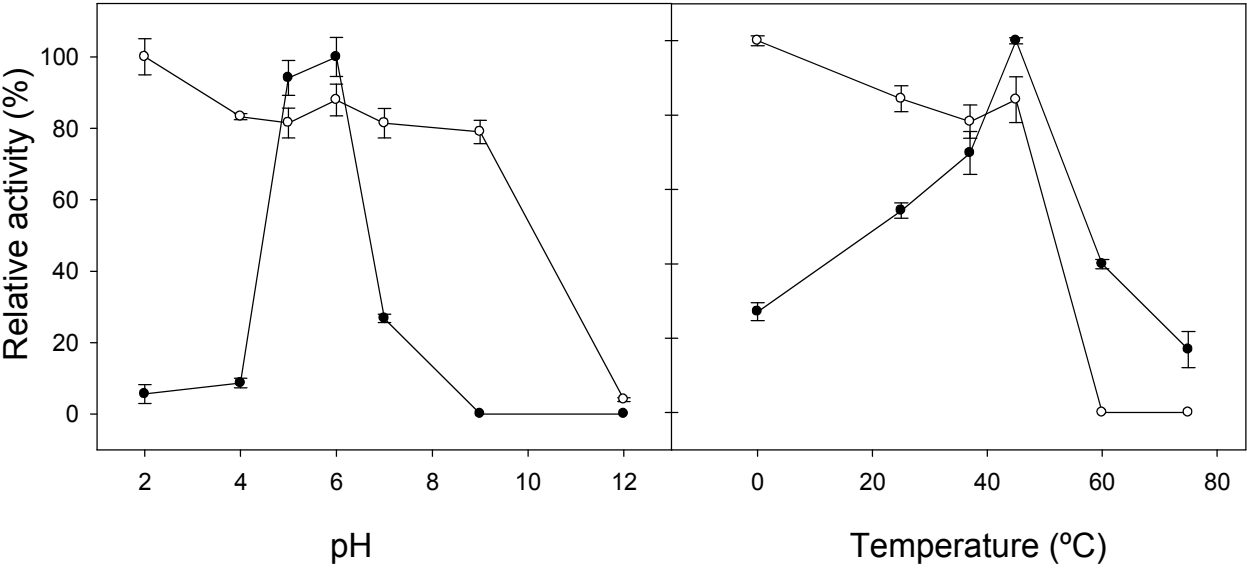


Figure 4

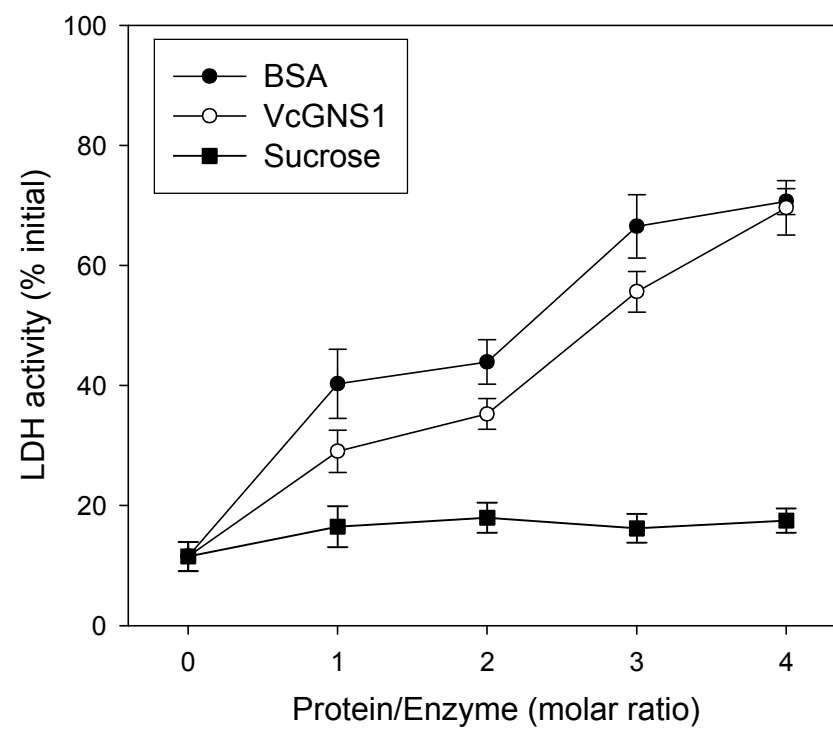


Figure 5

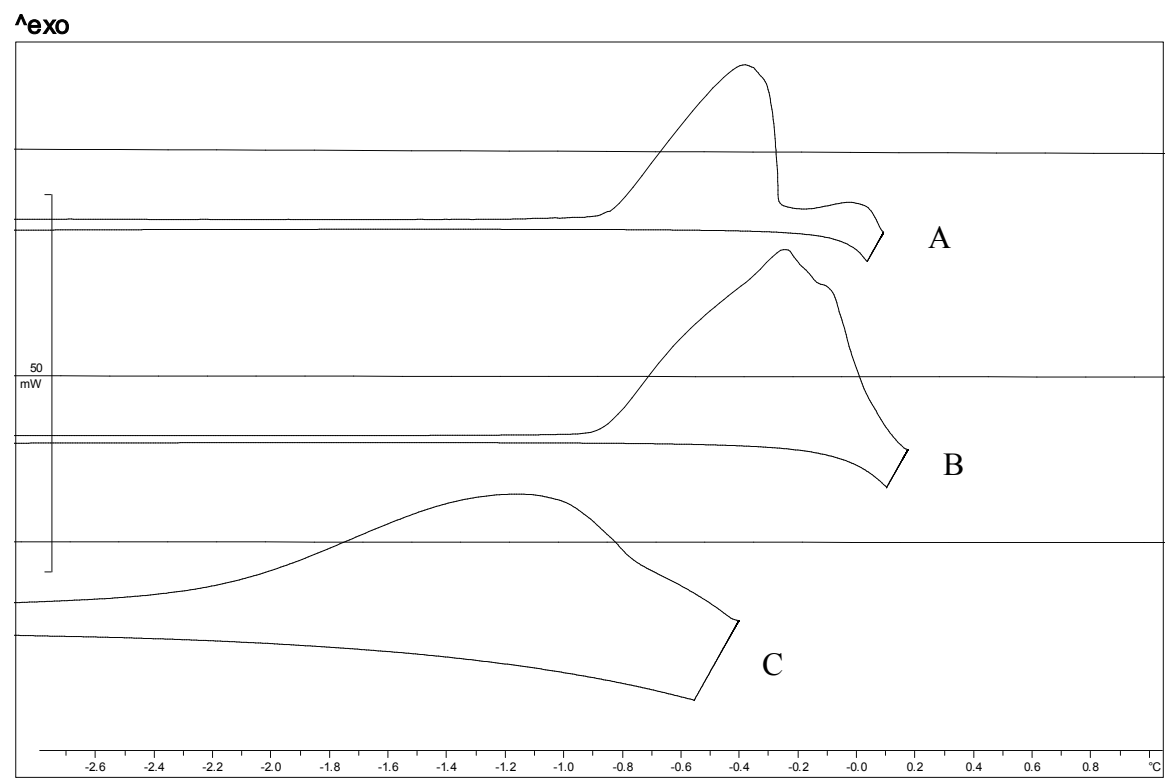


Table 1. Kinetic properties of recombinant VcGNS1 using *L. digitata* laminarin.

Spact ($\mu\text{mol min}^{-1} \text{mg}^{-1}$) ^a	9.70
K_m	
(mg mL^{-1})	0.78
(mM)	0.195
k_{cat} (s^{-1}) ^b	7.96
k_{cat}/K_m ($\text{s}^{-1} \text{mM}^{-1}$)	40.82
E_a (kJ mol^{-1}) ^c	19.95

^a Specific activity.
^b Catalytic constant rate (k_{cat}) = $V_{\text{max}}/[E]$, where $[E] = 0.025 \text{ nM}$.
^c Activation energy determined between 0 and 45 °C.

ARTÍCULO 7

Functionality of a class I chitinase from skin of grape berries.

Irene Romero, Carlos Fernandez-Caballero, M. Isabel Escribano, Carmen Merodio, M. Teresa Sanchez-Ballesta.

***Postharvest Biology and Technology.* Short Communication**
(pendiente de enviar)

RESUMEN

Hemos analizado cómo el almacenamiento a 0°C y altos niveles de CO₂ (20% CO₂ + 20% O₂) afectan a la expresión génica de una quitinasa de clase I (*VcCHIT1b*) en la piel de uvas de mesa (*Vitis vinifera* L. cv. Cardinal). El almacenamiento a bajas temperaturas durante 3 días indujo la expresión génica de *Vcchit1b* en uvas no tratadas. Por el contrario, el tratamiento de 3 días de CO₂ redujo el incremento en la acumulación de transcritos. Nosotros hemos sobreexpresado el cDNA de quitinasa de clase I en *Escherichia coli*. Debido a que la proteína se produjo en cuerpos de inclusión, la proteína fue solubilizada y replegada. La proteína recombinante mostró inhibición antifúngica contra *Botrytis cinerea* en estudios realizados con placas de agar. Además la proteína purificada VcCHIT1b exhibió una gran actividad crioprotectora para la enzima lábil a la congelación L-lactato deshidrogenase (LDH). Estos resultados sugieren que VcCHIT1b podría participar en la respuesta de las uvas de mesa para combatir las condiciones de bajas temperaturas y el ataque fúngico.

FUNCTIONALITY OF A CLASS I CHITINASE FROM SKIN OF GRAPE BERRIES

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Abstract

We have analyzed how low temperature (0 °C) storage and high CO₂ (20% CO₂ + 20% O₂) levels affect class I chitinase (*VcCHIT1b*) gene expression in the skin of table grapes (*Vitis vinifera* L. cv. Cardinal). Low temperature storage for 3 days induced *Vcchit1b* gene expression in non-treated grapes. By contrast, the 3-day treatment of high CO₂ levels reduced the increase in the transcript accumulation. We have overexpressed the chitinase class I cDNA in *Escherichia coli*. Since the protein was produced as insoluble inclusion bodies, the protein was solubilized and refolded. The recombinant protein showed antifungal inhibition against *Botrytis cinerea* in agar plates. Furthermore, the purified VcCHIT1b exhibited potent *in vitro* cryoprotective activity for the freeze labile L-lactate dehydrogenase (LDH) enzyme. These results suggest that VcCHIT1b may participate in the response of table grapes to combat low temperature conditions and fungal attack.

Keywords: Table grapes; Carbon dioxide; Chitinase; Gene Expression; Cryoprotective; Antifungal.

1. Introduction

Decay caused by *Botrytis cinerea* is responsible for most of the postharvest losses of table grapes during storage at low temperature (*Vitis vinifera* L.). This mold is controlled mainly by extensive use of fungicides. However, fungicides and chemical treatments may cause damage to grape berries if used excessively, and some consumers develop allergic reactions. Alternative gaseous methods such as controlled atmospheres and modified atmosphere packaging controlled table grapes postharvest decay (Crisosto et al., 2002; Artés-Hernández et al., 2004). In previous works, we showed the efficacy of a 3-day pretreatment with high CO₂ levels in maintaining the quality of the table grapes, and controlling the total decay (Romero et al., 2006). Likewise, high CO₂ treatment reduced the defence responses related to phenylpropanoid metabolism of table grapes in response to temperature shifts in the first stage of storage at 0°C (Sanchez-Ballesta et al., 2007). However, our previous studies indicated that the efficacy of high CO₂ pretreatment reducing total decay is not mediated by the induction of pathogenesis-related proteins (PRs) genes, such as class I chitinase and β -1,3-glucanase (Romero et al., 2006), indicating that factors other than fungal infection are involved in the induction of these genes in table grapes.

Chitinases catalyze the hydrolysis of chitin, a linear polymer of β -1,4-linked N-acetylglucosamine residues, which is a major structural component of the cell walls of many fungi. In plants, chitinases were induced upon invasion by pathogens and by a variety of abiotic stress factors (Collinge, 1993). Transgenic plants overexpressing chitinase and β -1,3-glucanase genes show enhanced resistance to fungal infection (Grison et al., 1996). A class II chitinase gene had important roles in bermudagrass in response to low temperature (de los Reyes et al., 2001). Likewise, class I and class II chitinases from winter rye were induced by low temperature and showed antifreeze

activity (Yeh et al., 2000). Although it has been reported the isolation of class I chitinase genes in grapes (Busam et al., 1997; Robert et al., 2002); only limited information is presently available on the regulation of gene expression in response to fungal attack. The aim of the present work was to analyze expression of a class I
5 chitinase gene in red table grapes exposed to low temperature and also assess how high CO₂ levels modulated its transcript accumulation. Likewise, we have investigated the possible physiological role of this protein in table grapes as antifungal and/or cryoprotectant, by the heterologous expression in *Escherichia coli*.

10 2. Material and Methods

Table grapes (*Vitis vinifera* L. cv. 'Cardinal') were harvested at random in Camas 5 (Sevilla, Spain) in July. After harvesting, the field-packaged bunches were transported to the laboratory where fruit were immediately forced-air precooled for 14 hours at -1 °C. After cooling, bunches free from physical and pathological defects were
15 randomly divided into two lots and stored at 0 ±0.5 °C and 95% relative humidity in two sealed neoprene containers of 1 m³ capacity. One lot was stored under a normal atmosphere for 6 days (non-treated fruit), and the other under a gas mixture containing 20% CO₂ + 20% O₂ + 60% N₂ (CO₂-treated fruit) for 3 days. The grapes were then transferred to air under the same conditions as non-treated fruit until the end of the
20 storage period. Berries from five clusters (approx. 300 g each cluster) were peeled, and the skin and pulp were frozen in liquid nitrogen, ground to a fine powder, and stored at -80 °C until analysis.

Total RNA extraction and northern blots were performed as described by Romero et al. (2006). Samples of denatured total RNA (10 µg) from the skin of grapes

were fractionated and blotted. Equal loading was confirmed by membrane staining with methylene blue. The *Vcchit1b* DNA probe was random primer labeled with $\alpha^{32}\text{P}$ -dCTP

The cDNA fragment of *Vcchit1b* (GenBank accession number DQ267094) without the N-signal peptide was amplified using forward primer (5'- ATT ATC GGA TCC GAG CAA TGT GGA GGG CAA GCT-3') and reverse primer (5'-GGC GAA TTC TTA GAT GGT GTC CAG CAG GAG-3') containing *Bam*HI and *Eco*RI restriction sites, respectively. The amplified DNA fragments were ligated into the multicloning sited of the pTrcHisA (Invitrogen, Carlstad, USA) previously digested with the same enzymes. The vector pTrcHisA-VcCCHIT1B were transformed into *E.coli* strain TOP10 cells, which were grown at 37 °C in LB-medium with 50 $\mu\text{g mL}^{-1}$ ampicillin and 0.8 mM glucose until the optical density at 600 nm reached 0.6 and then induced with 1 mM isopropyl- β -D-thiogalactoside (IPTG). After 4 h of induction at 37 °C, cells were harvested by centrifugation at 1760 x g for 20 min at 4 °C and frozen. The purification of VcCHIT1b was carry out by the method described by Kirubakaran et al. (2007), with slight modifications. Cells were disrupted with 1 g of glass beads (150-252 μm , Sigma) in a FastPrep machine (FP120, Bio101, Savant). The protein was properly renatured from inclusion bodies dialyzing gradually against denaturation-renaturation buffer (DR) containing progressively low concentrations of urea (6, 5, 4, 3, 2 and 1 mM) for 24 h each, finally using sterile distilled water. Protein concentration was determined by the method of Bradford (1976) using bovine serum albumin (BSA) as standard.

Protein analysis was performed on 12% sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE) using a Mini-Protean II Cell (Bio-Rad) equipment. The molecular mass of the separated polypeptides was estimated by

comparison to the mobility of pre-stained standard low molecular mass range proteins (Bio-Rad).

After a standard PAGE was performed, proteins were electro-transferred to PVDF membranes (Amersham) with a Mini Trans-Blot Cell (Bio-Rad). The Western blot was probed with a 1:5000 dilution of polyclonal anti-PRQ sera from tobacco, kindly provided by Dr. Fritig (Strasbourg, France) which were detected with a 1:5000 dilution of rabbit antiserum against IgG horseradish peroxidase conjugate (Amersham). The immuno-complexes were visualized using the enhanced chemiluminescence (ECL®) detection system (Amersham).

Recombinant purified VcCHIT1B were tested for antifungal activity against *Botrytis cinerea* (strain provided by the Spanish Type Culture Collection, Universidad de Valencia, Spain) by the hyphal extension-inhibition bioassay. The assay was carried out in 100 mm x 15 mm Petri plates containing 20 mL of potato dextrose agar (PDA). Freshly prepared inoculum (10 µL) was placed in the center and incubated for 24 h at 25 °C. After the mycelial colony had developed, sterile blank paper disks (0.7 cm in diameter) were placed around and at a distance of 1 cm away from the the mycelial colony. The disk assayed contained sodium acetate buffer 20 mM (control), an aliquot containing 25 µg of purified VcCHIT1b and an aliquot containing 200 µg of bacterial chitinase (*Streptomyces griseus*, Sigma). The plates were incubated for 35 h at 25 °C in the dark.

The *in vitro* cryoprotective activity was determined following the method described by Romero et al. (2007). Samples, either VcCHIT1b protein fractions or bovine serum albumin (BSA, Sigma, St. Louis, MO, USA), were diluted to varying concentrations and mixed with 2.364 µg of LDH from the stock solution. The resulting solution (300 µL) was frozen three times in liquid nitrogen for 30 s and then thawed at

room temperature for 5 min. LDH enzymatic activity was determined in aliquots of 30 μ L of the mixtures in a final volume of 1.5 mL of the reaction assay buffer (80 mM Tris-HCl pH 7.5, 100 mM KCl, 2 mM pyruvate and 30 mM NADH) at room temperature. NAD⁺ production was monitored as the decrease of absorbance at 340 nm for 4 min. Data is showed as the percentage of the activity present in unfrozen controls.

3. Results and Discussion

In previous work, we have isolated a full-length class I chitinase (*Vcchit1b*) cDNA from the skin of table grape (Romero et al., 2006) and our results indicated that the increase in *Vcchit1b* mRNA levels was paralleled by the change in total decay. To study the effect of low temperature storage and high CO₂ levels on *Vcchit1b* mRNA expression pattern, total mRNA from the skin of CO₂-treated and non-treated grapes stored at 0 °C was analyzed by northern hybridization. Low temperature increased the levels of the transcript after 3 and 6 days of storage in non-treated grapes. However, the increase in the accumulation of the *Vcchit1b* mRNA in the CO₂-treated grapes was lower and the transcript accumulation was not maintained when treated grapes were transferred to air for 3 days at 0 °C. In winter rye, transcription of a class I chitinase gene was responsive to cold temperature (Yeh et al., 2000). In this work, we observed that low temperature by itself has a clear effect on *Vcchit1b* gene expression and high CO₂ reduced this response.

To determine whether the *Vcchit1b* cDNA isolated encoded a protein with chitinase activity, and to analyze its functionality, the cDNA fragment corresponding to the mature protein was expressed in TOP10 *E. coli* cells as a pTrcHisA-VcCHIT1b fusion protein. The VcCHIT1b protein was induced in the presence of 1 mM IPTG at 37 °C for 4 h but we could not purificate the protein because it was aggregated as inclusion

bodies. It is known that recombinant proteins overexpressed in bacteria often form insoluble proteins that contain most of the expression protein (Marston, 1986). Hence, a class I chitinase from barley was produced as insoluble inclusion bodies by Kirubakaran et al. (2007). VcCHIT1b was solubilized and refolded from inclusion bodies by dialysis, and the purified recombinant protein showed a single protein band in SDS-PAGE (Fig. 2, lanes 2), suggesting that the native protein occurs as a monomer. Western blot analysis with an antiserum against tobacco PRQ showed a positive band with the same molecular mass (Fig. 2, lane 3).

We have analyzed the antifungal activity of the recombinant VcCHIT1b using the hyphal growth inhibition assay on agar plates with *B. cinerea* as the test fungus. The assays realized using 25 µg of purified VcCHIT1b showed inhibition of fungal growth (Fig. 3). This inhibition was higher than that observed for a commercial chitinase from *Streptomyces griseus*. These results agree with the studies showing the ability of classes I, IV and VI chitinases to inhibit growth of fungal hyphae *in vitro* (Derckel et al., 1998) or *in vivo*, in the case of class I chitinases (Benhamou et al., 1993).

We have investigated the ability of the recombinant chitinase to preserve LDH activity following freeze-thaw cycles in comparison with the level of cryoprotection provided by BSA. Without the addition of a cryoprotectant, three freeze-thaw cycles resulted in more than 80% of reduction of LDH activity (Fig. 4). Addition of VcCHIT1b or BSA, in protein:enzyme molar ratios from 0.25 to 1, significantly protected LDH activity. Recombinant VcCHIT1b was more efficient than BSA in protecting LDH at molar ratios from 0.25 to 2.5. At a molar ratio of 1, VcCHIT1b maintained 100% of initial LDH activity. By contrast, a tobacco class I chitinase did not demonstrate any cryoprotective effects, whereas glucanase of class I had potent

cryoprotective activity (Hinch et al., 1997). Likewise, a PR-5 protein from groundnut showed *in vitro* cryoprotective activity against LDH (Dave and Mitra, 1998).

In conclusion, present investigation reports the purification and characterization of a recombinant class I chitinase and the results indicated that VcCHIT1b displays activities as antifungal and potent cryoprotective.

Acknowledgements

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Figure Legends

Fig. 1. Effect of low temperature and high CO₂ levels on *VcChit1b* mRNA accumulation in the skin of 'Cardinal'. 10 µg of total RNA from the skin was fractionated by gel electrophoresis, blotted and hybridized with the *VcChit1b* probe. The equivalence of RNA loading of the lanes was demonstrated by methylene blue staining.

Fig. 2. (A) Recombinant VcCHIT1b protein was analysed by SDS-PAGE (12% polyacrylamide) and stained by Coomassie blue. Lanes 2 was loaded with 2 µg of reduced protein. Lane 1 was loaded with low molecular mass reference proteins and sizes are indicated on the left. (B) Immunoblot of a similar gel with reduced VcCHIT1b. The blot was incubated with polyclonal anti-PRQ sera from tobacco.

Fig. 3. Effect of recombinant chitinase from grape and bacterial chitinase on the mycelial growth of *Botrytis cinerea*. Position 1, control (Tris-HCl 50mM); 2, bacterial chitinase (200 µg); 3, Recombinant chitinase (25 µg). Photographs were taken after 48 h incubation.

Fig. 4. Cryoprotection of LDH by recombinant VcCHIT1b. A LDH solution was frozen with different concentrations of VcCHIT1b and BSA. The samples were thawed at room temperature and the LDH activity was measured. The relative activity represents the amount of LDH activity remaining after a freeze-thaw treatment as a percentage of the control enzyme activity. Error bars represent S.E (n=3).

Figure 1

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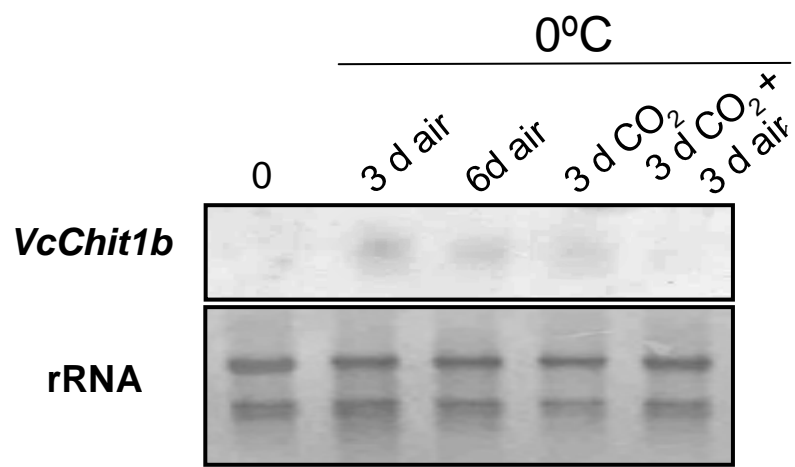


Figure 2

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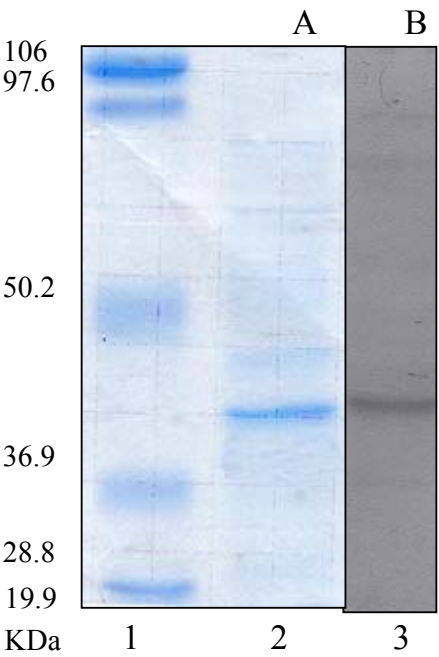
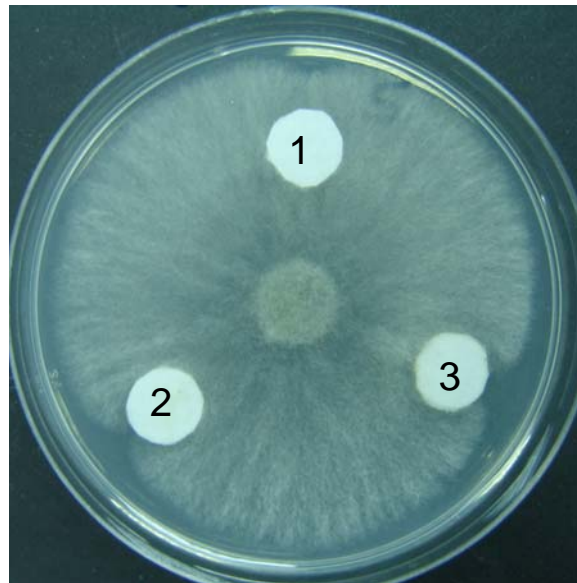


Figure 3

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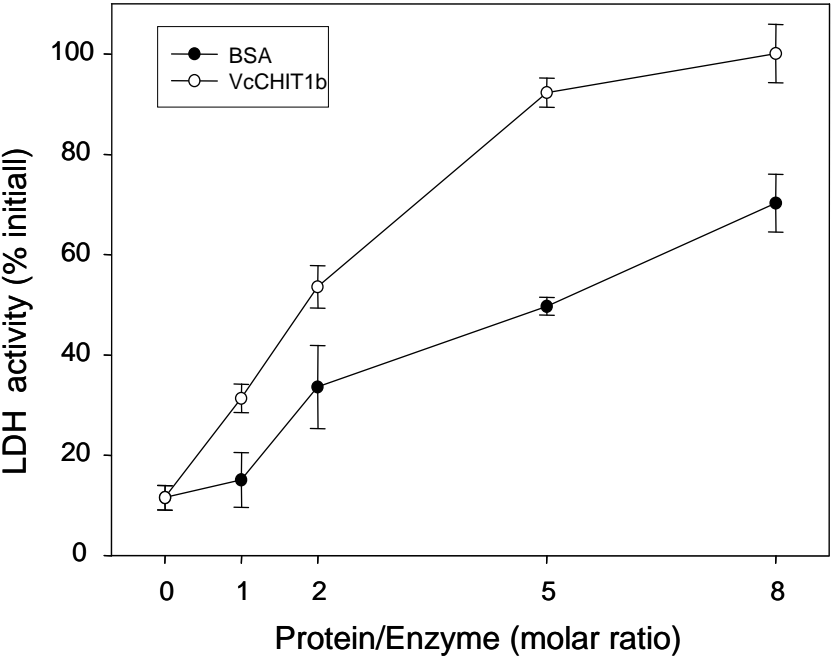


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Figure 4



Discusión

1. Análisis de la infección fúngica de la uva de mesa.

La infección por *Botrytis cinerea* es una de las principales causas de deterioro de uva de mesa durante su conservación postcosecha. Por tanto, uno de los parámetros indicadores de la eficacia de altos niveles de CO₂ y bajas temperaturas en la conservación de uva es el análisis del ataque fúngico. Observamos que la podredumbre aumentó gradualmente en las uvas no tratadas desde el inicio del periodo de conservación a 0°C. Por el contrario, en las uvas tratadas con CO₂, el ataque por hongos no apareció hasta después de 22 días de almacenamiento. Al final del periodo de conservación, la podredumbre observada en uvas no tratadas fue 5 veces superior a la de uvas tratadas. Resultados similares han sido descrito en uvas de mesa de cosecha temprana Redglobe, donde el desarrollo de *Botrytis* fue significativamente mayor en las bayas almacenadas en aire que en las conservadas mediante tratamientos con CO₂ (Crisosto et al., 2002).

En los ensayos sobre el periodo de vida útil de la uva durante la transferencia a 20°C tras 12 y 33 días de conservación, se observó que el porcentaje de granos infectados era también menor en los racimos tratados con un 20% de CO₂. Concretamente, cuando la transferencia a 20°C se realizó pasados 33 días de conservación, el ataque fúngico fue 2,1 veces inferior al observado en frutos no tratados. Por otro lado, cuando la transferencia a 20°C se realizó tras 12 días a 0°C, la incidencia del ataque por hongo no presentó cambios significativos en frutos no tratados; mientras que en las uvas tratadas el aumento observado fue de un 30%. También se ha descrito que concentraciones de CO₂ superiores a 10kPa controlaron la incidencia de podredumbres, independientemente de la concentración de O₂, en uva de mesa cv. Redglobe tras el periodo de vida comercial de 3 días (Crisosto et al., 2002).

2. Aislamiento y caracterización del gen que codifica una β -1,3-glucanasa de clase I.

El cDNA *VcGNS1*, que codifica una β -1,3-glucanasa de clase I, se aisló de piel de uva de mesa cv. Cardinal mediante RT-PCR y RACE 5'-3'. La secuencia deducida de aminoácidos de *VcGNS1* contiene un residuo de triptófano conservado implicado en la interacción con el sustrato de glucano (Ori et al., 1990), y un residuo de glutamato conservado, que se ha visto que actúa como nucleófilo en el mecanismo catalítico (Varghese et al., 1994). Asimismo, la secuencia deducida de aminoácidos contiene péptidos señal N- y C-terminal de 20 y 21 aminoácidos, respectivamente, presentes en las proteínas β -1,3-glucanasa de clase I. Estas proteínas son sintetizadas como preproteínas y las extensiones N- y C-terminal son eliminadas durante o después del transporte de la proteína a la vacuola (Shinshi et al., 1988).

2.1. Estudio de la expresión de β -1,3-glucanasa de clase I durante la conservación de uva a 0°C.

En frutos no tratados, el incremento en la acumulación de los niveles de mRNA *VcGNS1* después de 12 días de conservación a 0°C fue similar al observado al final de la conservación. Por el contrario, para el mismo periodo de tiempo, el incremento en el porcentaje de granos dañados por hongo fue 4 veces superior al final del almacenamiento. En los frutos tratados con CO₂, se observa incluso un descenso en los niveles de acumulación del mRNA *VcGNS1* al tiempo que se detectó un incremento significativo del ataque fúngico. Esta aparente falta de correlación entre los niveles de expresión génica de *VcGNS1* y el ataque fúngico, podría indicar que otros factores distintos de la infección por hongos están involucrados en su inducción. Se ha descrito la inducción de β -1,3-glucanasas en hojas de vid tras la infección por *B. cinerea* (Renault et al., 1996) así como un aumento en los niveles de los transcritos de una glucanasa en hojas de vid infectadas

por *Uncinula necator* y en bayas inmaduras (Jacobs et al., 1999). También se ha descrito la acumulación de glucanasas en respuesta a otros estreses. Así, se ha observado un aumento en la acumulación de mensajeros de una β -1,3-glucanasa de clase II de tomate y de una β -1,3-glucanasa de clase III de mandarina, durante el almacenamiento a bajas temperaturas de estos frutos (Ding et al., 2002; Sanchez-Ballesta et al., 2006).

Con el fin de estudiar el efecto de la conservación a 0°C en la inducción de *VcGNSI*, se analizó la acumulación de mensajeros al comienzo de la conservación. Se observó que las bajas temperaturas afectaban a la expresión génica de *VcGNSI* independientemente del ataque fúngico. Así, después de 3 días a 0°C, se observó un gran aumento en los niveles del mRNA *VcGNSI* en la piel de uvas no tratadas, que se mantuvo después de 6 días. Por el contrario, el tratamiento con CO₂ redujo la acumulación del transcrito observada a 0°C, mientras que se detectó un ligero aumento en los niveles cuando las uvas tratadas fueron transferidas a aire. Asimismo, la actividad glucanasa aumentó en respuesta a las bajas temperaturas, aunque no se observaron diferencias significativas entre frutos tratados y no tratados. Existen numerosos estudios que relacionan la inducción de actividad β -1,3-glucanasa en tejidos vegetativos de plantas en respuesta a estreses abióticos y a la infección por distintos hongos (Fanta et al., 2003; Cota et al., 2007). Lawrence et al. (2000) encontraron niveles de actividad β -1,3-glucanasa superiores en tomates resistentes a la infección fúngica comparados con tomates susceptibles, y estos niveles aumentaron en ambos casos tras la inoculación con el hongo *Alternaria solani*. También se ha descrito un aumento en la actividad β -1,3-glucanasa en respuesta a la infección por *Alternaria alternata* en los cultivares de tomate Sunpride, Jerónimo y Charleston (Cota et al., 2007). Sin embargo, nuestros resultados apuntan a que la β -1,3-glucanasa podría estar implicada en la respuesta de la uva a las bajas temperaturas

independientemente del ataque fúngico. Se han descrito previamente β -1,3-glucanasas ácidas y básicas de centeno que fueron activas frente al frío y que mantuvieron actividad hidrolítica parcial a temperaturas por debajo de 0°C (Yaish et al., 2006).

2.2. Expresión, purificación y caracterización de la β -1,3-glucanasa de clase I.

Con el objetivo de determinar si el cDNA *VcGNS1* aislado de uva de mesa codifica una proteína con actividad glucanasa, y analizar su funcionalidad *in vitro*, se llevó a cabo la expresión de la proteína en el sistema pTrcHIS en *E. coli*. La proteína recombinante purificada mostró una única banda en geles de SDS-PAGE, y la masa molecular de la proteína recombinante fue de aproximadamente 40 kDa. El aumento observado en la masa molecular de la glucanasa recombinante con respecto al valor teórico (34,6 kDa) es debido a la cola de poli-histidinas que se agregó a la secuencia completa, necesaria para la purificación en columnas de afinidad. La mayoría de las β -1,3-glucanasas caracterizadas pertenecen a una familia de proteínas con una masa molecular de 33-36 kDa, cuya estructura tridimensional, bien sea conformación $(\beta/\alpha)_8$ o estructura en TIM-barril, y actividad enzimática han sido bien establecidas (Varghese et al., 1994; Chen et al., 1995). Sin embargo, existe un número limitado de β -1,3-glucanasas con extensión C-terminal que han sido descritas (Hird et al., 1993; Futamura et al., 2000). Los ensayos de actividad mostraron que la proteína recombinante presenta actividad β -1,3-glucanasa hidrolizando el sustrato laminarina con un pH óptimo de 6, ligeramente superior al determinado en otras proteínas β -1,3-glucanasa (Churngchow et al., 1995; Dicko et al., 2001), pero con una temperatura óptima similar de 45°C. Cabe destacar que *VcGNS1* fue activa en un amplio rango de temperaturas, presentando mayor termoestabilidad que las β -1,3-glucanasas de *Boscia senegalensis* (Dicko et al., 2001) y cebada (Hrmova y Fincher, 1993). Además, la

proteína recombinante presentó a 0°C un 27% de actividad relativa y la mayor termoestabilidad después de 1 hora de incubación sin sustrato.

Analizando los parámetros cinéticos de la proteína VcGNS1 se observó que la energía de activación E_a fue menor que los valores obtenidos para otras hidrolasas de carbohidratos (Dicko et al., 2001), y constante en el rango de temperaturas estudiado. Es importante destacar que en frutos, no se ha descrito hasta el momento una β -1,3-glucanasa con valores tan bajos de E_a que presente actividad hidrolítica a bajas temperaturas. En cuanto a los parámetros cinéticos, la K_m de la β -1,3-glucanasa fue mayor (0.195 μ M) que las descritas para β -1,3-glucanasas de otras plantas (Akiyama et al., 1997; Dicko et al., 2001), mientras que fue del orden de las K_m encontradas en las isoenzimas de β -1,3-glucanasas (GI, GII, y GIII) aisladas de hojas de cebada (Hrmova y Fincher, 1993). Sin embargo, la constante catalítica (K_{cat}) presentó un valor (7.96 s^{-1}) que fue significativamente menor que el de otras glucanasas de plantas (Hrmova y Fincher, 1993; Akiyama et al., 1997). Por otro lado, los resultados indican que VcGNS1 podría tener un comportamiento de endo-hidrolasa ya que no se observó efecto inhibitor de la δ -gluconolactona (potente inhibidor de exoglucanasas) en la actividad enzimática. Este comportamiento se ha observado también en otras glucanasas aisladas (Vogelsang y Barz, 1993; Morohashi y Matsushima, 2000).

2.3. Estudio de la funcionalidad de la β -1,3-glucanasa recombinante.

En cuanto a la funcionalidad de la β -1,3-glucanasa de clase I, se analizó su posible papel como anticongelante y/o crioprotectora. Se han descrito PRs de centeno que actúan como anticongelantes durante la aclimatación al frío (Hon et al., 1995). De hecho, Yaish et al. (2006), expusieron la hipótesis de que glucanasas recombinantes de centeno podrían

actuar como anticongelantes participando en la inhibición de la formación de cristales alargados de hielo, y siendo capaces de degradar glucanos a bajas temperaturas. Sin embargo, nuestros análisis de la actividad anticongelante donde se midió la actividad de histéresis térmica mediante DSC determinaron que VcGNS1 no presentó dicha capacidad. Por otro lado, distintos estudios de la actividad crioprotectora de β -1,3-glucanasas, han mostrado que no es un efecto general de las mismas. Así, en hojas de espinaca y repollo, proteínas β -1,3-glucanasas se acumularon durante la aclimatación al frío, y una glucanasa de clase I tuvo potente actividad crioprotectora (Hincha et al., 1997); mientras que una β -1,3-glucanasa recombinante de clase III de mandarinas sensibles al frío mostró actividad glucanasa pero no crioprotectora (Sanchez-Ballesta et al., 2006). Sin embargo, en este estudio, se ha demostrado que la VcGNS1 tiene actividad crioprotectora frente a la proteína lábil LDH. Los valores de crioprotección observados para VcGNS1 fueron similares a los descritos para la proteína BSA (del inglés *Bovine Serum Albumin*), conocida estabilizadora de proteínas (Tamiya et al., 1985). Se han observado resultados similares en WAP18, una PR10 de mora (Ukaji et al., 2004) y COR15am, una proteína tipo LEA de *Arabidopsis* (Artus et al., 1996) entre otras. Por el contrario, también existen proteínas con actividad crioprotectora que presentan valores superiores a los del BSA. Es el caso de COR85 y PCA60, dehidrinas inducidas por frío con actividades crioprotectoras 4 y 2 veces superiores a las encontradas para el BSA (Kazuoka y Oeda, 1994; Wisniewski et al., 1999). El porcentaje de residuos polares en VcGNS1 es de 40% como ocurre en la proteína WAP18 (Ukaji et al., 2004) y estos autores indican que la baja capacidad crioprotectora encontrada en esta proteína en comparación con otros crioprotectores, puede ser debido a la baja relación de residuos polares en la superficie de la proteína.

3. Aislamiento y caracterización del gen que codifica una quitinasa básica de clase I.

El cDNA *VcCHIT1b* que codifica una quitinasa básica de clase I se aisló de piel de uva de mesa cv. Cardinal mediante RT-PCR y RACE 5'-3'. El análisis de la secuencia de aminoácidos deducida mostró que la proteína VcCHIT1b está compuesta por tres dominios presentes en las quitinasas de clase I: un dominio N-terminal de unión a quitina rico en cisteínas, una región bisagra rica en prolinas y un dominio catalítico altamente conservado. Además, también presenta una extensión C-terminal requerida para la localización vacuolar de la proteína (Di Sansebastiano et al., 1998). El hecho de que la proteína deducida VcCHIT1b presentara una homología del 100% con la quitinasa vacuolar de clase I de hojas de *V.vinifera* cv. Ugni Blanc (Robert et al., 2002) y a la de cultivos celulares de *V.vinifera* cv. Pinot Noir (Busam et al., 1997) hace pensar que las quitinasas de clase I estén muy bien conservadas en las especies de *Vitis*.

3.1. Estudio de la expresión de la quitinasa de clase I durante la conservación de uva a 0°C.

La acumulación de transcrito *VcCHIT1b* durante la conservación de las bayas a bajas temperaturas fue paralela a la evolución del ataque fúngico que tuvo lugar después de 12 días y que incrementó con el tiempo de almacenamiento. Sin embargo, en las uvas tratadas con CO₂, se detectó un incremento en la expresión génica de la quitinasa de clase I después de 22 días de almacenamiento al tiempo que se observó la aparición de podredumbre en los frutos. Estos resultados muestran una relación entre la acumulación del transcrito *VcCHIT1b* y la evolución de la podredumbre. Se han descrito quitinasas de clase III de calabaza (Métraux et al., 1989) y tabaco (Lawton et al., 1992) que se inducen como respuesta a la infección por patógeno. En cultivos celulares de *V. vinifera* cv. Pinot Noir se observó un aumento en la expresión de una quitinasa de clase III en respuesta a

elicitores fúngicos y bacterianos (Busam et al., 1997). Asimismo, se observó un aumento en la quitinasa básica de clase I aislada de hojas de *V. vinifera* cv. Pinot Noir parcialmente infectadas por *B. cinerea*, siendo los niveles del mensajero más elevados a mayor grado de infección fúngica (Bézier et al., 2002).

En cuanto a la actividad quitinasa, se observaron dos picos de mayor actividad a los 12 y a los 28 días en uvas no tratadas. Sin embargo, en frutos tratados el incremento se observó a los 22 días y fue significativamente menor que los observados en uvas no tratadas. En hojas de vid de cv. Sultana y cv. Cabernet Sauvignon se observó que la actividad quitinasa incrementaba proporcionalmente a la evolución del ataque fúngico de *U. necator* (Jacobs et al., 1999). Asimismo, Salzman et al., (1998) observaron la acumulación de actividad quitinasa en uvas cv Concord, en respuesta a la infección por *B. cinerea*.

El análisis de la expresión génica de *VcCHIT1b* durante la fase inicial del periodo de conservación a bajas temperaturas, mostró que en uvas no tratadas, los niveles del mensajero aumentaban tras 3 y 6 días de almacenamiento a 0°C. Sin embargo, en uvas tratadas se observó un aumento en los niveles de expresión al finalizar el tratamiento de 3 días, pero no se mantuvo cuando las uvas fueron transferidas a aire. Teniendo en cuenta que nuestros resultados indican que el ataque por hongo comenzó a partir de los 12 días en uvas no tratadas y de los 22 días en uvas tratadas, la acumulación de mRNA de *VcCHIT1b* observada los primeros días de almacenamiento, principalmente en uvas no tratadas, podría ser una respuesta a las condiciones ambientales de conservación. Una proteína de 35 kDa que se acumuló a bajas temperaturas en el apoplasto de hojas de centeno, fue purificada y presentó tanto actividad endoquitinasa como antifúngica, probando que se trataba de una enzima con doble función (Hon et al., 1995).

3.2. Estudio de la expresión de la quitinasa de clase I durante el periodo de vida comercial de uva a 20°C.

Uvas conservadas a bajas temperaturas experimentan un rápido deterioro, principalmente causado por el ataque de patógenos, cuando son transferidas a temperatura ambiente (Crisosto et al., 2002). De ahí, la importancia de conocer y estudiar los cambios moleculares durante su periodo de vida comercial. Tras el paso a 20°C después de 33 días de conservación, se observó un aumento brusco en la acumulación de mRNA de *VcCHIT1b* tanto en uvas tratadas como no tratadas, siendo los niveles de expresión similares en ambos casos. También la podredumbre causada por el hongo aumentó tanto en uvas tratadas (3,8 veces) como en no tratadas (1,76 veces) durante el periodo de vida comercial a 20°C. Sin embargo, en términos globales, el ataque fúngico fue 2,2 veces menor en uvas tratadas que en no tratadas al final de la conservación. Por otro lado, se ha observado un control efectivo contra *B. cinerea* y *Penicillium digitatum* por medio de la combinación de quitinasas mezcladas con otros compuestos antifúngicos (Ali et al., 2003). En este sentido, nuestros resultados han mostrado altos niveles de actividad quitinasa a los 12 días, y tras el paso a 20°C, principalmente en uvas tratadas, que podría asociarse a la menor incidencia de ataque fúngico observado en las bayas. Sin embargo, durante el periodo de vida útil estudiado al final de la conservación, observamos que mientras en frutos no tratados la actividad quitinasa disminuyó drásticamente alcanzando valores incluso un 45% por debajo de los cuantificados en uvas recién traídas de campo, en las bayas tratadas con CO₂ aumentó alrededor de un 73% con respecto a los valores observados antes del paso a 20°C. Esta aparente falta de correlación entre los niveles transcripcionales de *VcCHIT1b* y de actividad quitinasa observado durante el periodo de vida comercial tras 33 días de conservación en uvas no tratadas, podría explicarse en términos de cambios en propiedades cinéticas y reguladoras de la enzima quitinasa por

efecto de las bajas temperaturas. Distintos factores, incluyendo modificaciones post-transcripcionales podrían estar implicados en la modulación de la actividad quitinasa.

3.3. Expresión y purificación de una quitinasa de clase I.

La secuencia correspondiente a la proteína quitinasa madura, sin el extremo N-terminal fue expresada en células de *E. coli* TOP 10 como una proteína de fusión pTrcHisA-VcCHIT1b. Durante la inducción de la proteína recombinante se formaron cuerpos de inclusión, por lo se llevo a cabo la solubilización y renaturalización *in vitro* para posteriores análisis. Los cuerpos de inclusión son agregados heterogéneos de elevada densidad, formados por diversas proteínas que poseen cierta estructura secundaria (Carrió et al., 2000). Aunque la expresión de proteínas en la forma de cuerpos de inclusión es a menudo considerada indeseable, su formación puede ser ventajosa, ya que su aislamiento del homogeneizado celular es una manera conveniente y efectiva de purificar la proteína de interés (Surinder y Amulya, 2005). La formación de los cuerpos de inclusión es independiente del huésped empleado para expresar una proteína, ya que se han obtenido incluso cuando se expresa una proteína endógena (expresión homóloga). Tampoco hay una relación directa entre la formación de los cuerpos de inclusión y las características intrínsecas de la proteína, como por ejemplo el peso molecular y la hidrofobicidad. Sólo en el caso de que la proteína forme puentes disulfuro en su estructura, como puede ser el caso de VcCHIT1b con un dominio N-terminal rico en cisteínas, se ha visto cierta relación entre ambos parámetros (Lilie et al., 1998). Hasta el momento sólo se ha descrito la expresión y purificación de una quitinasa recombinante de clase I de cebada que formó cuerpos de inclusión (Kirubakaran et al., 2007). En los últimos años, se han desarrollado métodos novedosos para replegar proteínas con el fin de renaturalizar las proteínas de los cuerpos de inclusión (Tsumoto et al., 2003; Vallejo y Rinas, 2004; Middelberg, 2004). Estos incluyen

tres métodos como son dilución, diálisis o separación en fase sólida (Clark, 1998). Entre los distintos métodos existentes se utilizó la diálisis frente a distintos tampones con concentraciones decrecientes de urea. La quitinasa recombinante purificada mostró una única banda en geles SDS-PAGE. La masa molecular de la quitinasa recombinante se determinó en 34,6 kDa por comparación de su movilidad relativa en geles SDS-PAGE con las de proteínas estándar. Estos resultados se corroboraron mediante Western Blot con antisuero anti PRQ. Se observó un ligero aumento en la masa molecular respecto al valor teórico (31,27 kDa) debido, igualmente, a la cola de poli-histidinas que se agregó a la secuencia completa y que resultaba necesaria para su posterior purificación.

3.4. Estudio de la funcionalidad de la quitinasa recombinante.

La funcionalidad *in vitro* de la quitinasa de clase I también fue estudiada. Se analizó la actividad antifúngica de la VcCHIT1b por inhibición de crecimiento de las hifas de *B. cinerea* sobre placas de agar dextrosa. Utilizando 25 µg de la proteína purificada se observó inhibición del crecimiento del hongo. Esta inhibición fue superior que la observada utilizando quitinasa comercial de *Streptomyces griseus*. Estos resultados están de acuerdo con estudios realizados con quitinasas de clase I, IV y VI en los que se ha observado que estas proteínas son capaces de inhibir el crecimiento de las hifas *in vitro* (Collinge et al., 1993; Derckel et al., 1998) o incluso *in vivo*, en el caso de la quitinasa de clase I (Benhamou et al., 1993). Resultados similares se han observado con endoquitinasas aisladas de granos de maíz, trigo y cebada, que fueron capaces de inhibir la elongación de las hifas del test de hongos (Roberts y Selitrnnikoff, 1988). La combinación de una quitinasa de uva y una osmotina, fue efectiva inhibiendo el crecimiento del micelio de *B. cinerea* (Salzman et al., 1998). Además, la proteína recombinante de quitinasa de clase I de

cebada mostró actividad antifúngica *in vitro* frente a seis hongos fitopatógenos, entre los que también se encontraba *B. cinerea* (Kirubakaran et al., 2007).

Cabe destacar la elevada capacidad crioprotectora de la quitinasa recombinante frente a la proteína LDH utilizando BSA como control. Se ha mostrado que la proteína recombinante VcCHIT1b es más eficiente que el BSA protegiendo la LDH; observándose a la relación molar de 1, que la quitinasa recombinante era capaz de recuperar el 100% de la actividad LDH inicial. Se han descrito distintas proteínas PR inducidas por bajas temperaturas (Tronsmo et al., 1993; Zhu et al., 1993; Gatschet et al., 1993); y algunas de ellas presentan capacidad crioprotectora, como es el caso de la PR 10/Bet v1 de mora (Ukaji et al., 2004).

En algunos frutos, se ha observado una relación entre la aclimatación al frío, la adquisición de capacidad crioprotectora y la tolerancia a la congelación (Ukaji et al., 2004; Griffith et al., 1997). Se han descrito quitinasas en centeno inducidas en respuesta a bajas temperaturas y que mostraban capacidad anticongelante (Hon et al., 1995). Asimismo, se han caracterizado dos quitinasas que se acumulan en hojas de centeno durante la aclimatación al frío, que también presentaban actividad anticongelante (Yeh et al., 2000). Sin embargo, la quitinasa recombinante de este estudio, VcCHIT1b, no presentó capacidad anticongelante analizando la actividad de histéresis térmica mediante DSC.

Discusión general

1. Efecto de la aplicación de elevadas concentraciones de CO₂ en los cambios metabólicos asociados con la respuesta de uva de mesa a 0°C.

La aplicación de un 20% de CO₂ durante 3 días evitó los cambios metabólicos asociados con la respuesta de uva de mesa en la fase inicial de conservación a 0°C. En la pulpa, estos cambios se centraron principalmente en un aumento de SSC y pH, así como en un descenso de TA en comparación con los valores de los frutos recién traídos de campo. En la piel de la uva, los cambios se concretaron en un aumento significativo tanto del contenido de antocianos totales medido por el método diferencial de pH, como del calculado a partir de la suma de antocianos individuales cuantificados por HPLC-DAD-MS. Se ha descrito previamente, que el contenido de antocianos aumenta en frutos durante la conservación postcosecha a bajas temperaturas (Kalt et al., 1999; Lo Piero et al., 2005; Stiles et al., 2007). El incremento de antocianos se ha intentado correlacionar en distintos estudios con el aumento en la capacidad antioxidante (Wang y Lin, 2000; Jakobek et al., 2007). Sin embargo, debido a que en un mismo extracto puede haber numerosos compuestos antioxidantes con distintos mecanismos de acción y entre los que, además, se pueden establecer reacciones sinérgicas, todavía no existe un consenso sobre cual sería el método más adecuado para efectuar el cálculo de la capacidad antioxidante. Todo ello, unido al elevado número de técnicas empleadas en los trabajos publicados, dificulta la comparación de resultados. En este trabajo se ha empleado el método ABTS, uno de los más empleados en la literatura, para la evaluación de la capacidad antioxidante (Miller et al., 1996; De Beer et al., 2006; Ozgen et al., 2006). Además, considerando que las reacciones que se llevan a cabo para determinar la capacidad antioxidante son fuertemente dependientes del pH (Borkowski et al., 2005; Pérez-Jiménez et al., 2006), la evaluación de la capacidad antioxidante realizada a los extractos se completó con la determinación de la TAC calculada a partir de la suma de la contribución individual de cada antociano. Los

resultados han mostrado un incremento en la capacidad antioxidante de los extractos de piel de uva después de 3 días de conservación a 0°C paralelo al aumento en la acumulación de cada uno de los antocianos identificados en esta variedad. El aumento en la capacidad antioxidante de los extractos de uvas no tratadas se debió principalmente a la contribución de la peonidina-3-G, el antociano mayoritario de este cultivar.

El CO₂ evitó el incremento transitorio en el contenido de antocianos totales e individuales. Al finalizar el tratamiento con un 20% de CO₂ la piel de los frutos presentó un valor de la TAC calculada similar a la de los frutos recién cosechados. También se ha descrito en frutos almacenados en CA una menor actividad antioxidante (Van der Sluis 2001; Remón et al., 2004). El estudio detallado del perfil de antocianos en los frutos al finalizar el tratamiento gaseoso permite concluir que los altos niveles de CO₂ evitaron la acumulación de peonidina-3-G y el consiguiente incremento en la capacidad antioxidante. Por el contrario, el tratamiento gaseoso potenció la acumulación de antocianos minoritarios como la pelargonidina-3-G al tiempo que redujo la acumulación de delfinidina-3-G. El descenso significativo en este antociano al finalizar el tratamiento y durante los primeros días de transferencia al aire podría estar relacionado con la mayor pérdida de tonalidad azul-morada observada en los frutos tratados con CO₂, tal y como muestran los valores del ángulo hue; así como con la menor capacidad antioxidante encontrada en estos frutos.

En relación con el metabolismo de los fenilpropanoides, también se ha comprobado que al finalizar el tratamiento gaseoso de 3 días el contenido en *trans*-resveratrol era menor que en los extractos de piel de frutos mantenidos en aire a 0°C. Más aún, el menor incremento en el contenido de antocianos y el descenso de *trans*-resveratrol observados en uva de mesa cv. Cardinal en respuesta a las elevadas concentraciones de CO₂, se ha relacionado con la menor expresión de genes que codifican enzimas clave en la síntesis de estos compuestos como la PAL, CHS y STS.

La inducción de la expresión de PRs, otra de las respuestas observada frente a las bajas temperaturas, también se vio atenuada en los frutos al finalizar el tratamiento gaseoso. Desde el comienzo del almacenamiento a 0°C se observó un aumento en los niveles de expresión de los genes de β -1,3-glucanasa y quitinasa, siendo mayor en β -1,3-glucanasas. Dado que existía en la bibliografía información sobre la función de β -1,3-glucanasas y quitinasas de otras plantas como crioprotectoras, anticongelantes (Hincha et al., 1997; Yeh et al., 2000; Ukaji et al., 2004; Yaish et al., 2006) y/o antifúngicas (Hon et al., 1995; Derckel et al., 1998; Kirubakaran et al., 2007), se procedió a estudiar la funcionalidad de las proteínas recombinantes obtenidas por expresión heteróloga. Se observó que las dos proteínas recombinantes purificadas presentaban capacidad crioprotectora; en concreto, la β -1,3-glucanasa presentó una actividad crioprotectora del orden del BSA, mientras que la quitinasa mostró una actividad crioprotectora hasta 2,5 veces superior al BSA en una relación equimolar de proteína/LDH. Sin embargo, ambas proteínas recombinantes no mostraron actividad anticongelante.

2. Efecto residual del CO₂ en la mejora de la uva de mesa, con respecto al ataque por hongo, a través del metabolismo de los fenilpropanoides y PRs.

Durante la transferencia al aire después de 3 días de tratamiento se confirmó el efecto beneficioso de los altos niveles de CO₂ en el mantenimiento de la calidad de la uva de mesa a lo largo de la conservación a 0°C. Los resultados indican que los racimos tratados con CO₂ presentaron una menor pérdida de peso, así como un menor marchitamiento y oscurecimiento del raquis que los racimos no tratados. Crisosto et al. (2002) describieron signos de marchitamiento del raquis al aplicar altos niveles de CO₂ (15 kPa) dependiendo del estado de desarrollo del fruto. Además, al ser un tratamiento de corta duración, se evitó la aparición de olores y sabores extraños que se pueden producir en condiciones de hipoxia

(Kader, 2002). Los resultados también indican que no se produjeron pardeamientos en la pulpa de las bayas tratadas. Además, los frutos tratados con CO₂ presentaron una significativa menor pérdida de acidez que los no tratados después de 33 días de conservación a 0°C, lo que explica su menor índice de madurez (SSC/TA).

Fundamentalmente, el empleo de altos niveles de CO₂ redujo y retrasó la aparición de podredumbre en las uvas de mesa. Al final de la conservación a 0°C, se observó una disminución significativa de los granos infectados por hongos en uvas tratadas con CO₂. Estudiando el posible papel de la ruta de los fenilpropanoides en esta mejora de la calidad de la uva, se observó que los niveles de expresión de *PAL*, *CHS* y *STS* fueron menores en uvas tratadas con CO₂ que en uvas no tratadas. Además, los niveles de antocianos al final de la conservación fueron similares a los de los frutos recién traídos de campo y, tampoco se observaron diferencias significativas en la capacidad antioxidante. Por otro lado, se analizaron los niveles de *trans*-resveratrol en la piel de la uva a lo largo de la conservación. En uva cv. Cardinal el contenido de esta fitoalexina en frutos recién traídos de campo fue de 44,11 µg/g peso fresco. Se ha descrito que el resveratrol se acumula en respuesta a estreses bióticos y abióticos (Liswidowati et al., 1991; Adrian et al., 1998; Cantos et al., 2000). En los ensayos realizados, se observó un incremento significativo en los niveles de *trans*-resveratrol en las uvas no tratadas al final de la conservación coincidiendo con el mayor porcentaje de podredumbre. Por otro lado, el descenso observado en los niveles de *trans*-resveratrol al final del tratamiento gaseoso fue incrementando progresivamente después de la transferencia al aire alcanzando, a los 33 días, valores similares a los de los frutos recién cosechados.

En cuanto a las PRs, se ha descrito el papel de las quitinasas y β -1,3-glucanasas frente al ataque por patógenos (Kim y Hwang, 1994; Salzman et al., 1998). Los resultados muestran una menor acumulación del mRNA de la glucanasa en las uvas tratadas con CO₂

respecto a las no tratadas a lo largo de la conservación. Por el contrario, los niveles de expresión del mRNA de la quitinasa fueron similares en ambos casos aunque se observó un retraso en su inducción en las uvas tratadas. Asimismo, este retraso coincidió con el observado en el desarrollo de la podredumbre. Estudiando la funcionalidad de las dos enzimas, se observó que la β -1,3-glucanasa no presentó, por sí misma, actividad antifúngica frente *B. cinerea* en ensayos *in vitro*. Se ha descrito que la combinación con otras PRs puede tener un efecto sinérgico y potenciar la respuesta antifúngica (Mauch et al., 1988). En este trabajo, se observó un efecto sinérgico cuando la β -1,3-glucanasa se ensayó junto con una quitinasa bacteriana de *S. griseus* (datos no publicados). Sin embargo, la quitinasa sí presentó capacidad antifúngica frente *B. cinerea* a las concentraciones ensayadas.

Conclusiones

1. Los datos obtenidos apuntan a la utilidad comercial del tratamiento de 3 días con altos niveles de CO₂ durante la conservación a 0°C para mantener la calidad inicial de uva de mesa cv. Cardinal. Así, se observó un mantenimiento de la acidez, una menor pérdida de peso y una disminución del marchitamiento del raquis.

2. Los resultados fisiológicos y moleculares indican que durante la fase inicial de conservación a 0°C, la uva de mesa induce mecanismos orientados hacia una superación del estrés oxidativo que no se manifiestan con la misma intensidad en uvas tratadas con CO₂ durante 3 días. La protección inducida por el CO₂ se puede observar previamente a la transferencia al aire analizando el contenido total e individual de antocianos.

3. La respuesta a las bajas temperaturas de conservación es transitoria como lo demuestra la recuperación de los valores iniciales de sólidos solubles, antocianos totales, y de los niveles de expresión de los mensajeros de la *PAL* y *CHS*. Este efecto se evita al menos parcialmente con el tratamiento de CO₂, cuyo efecto beneficioso se mantiene hasta el día 22 de la conservación, disminuyendo a partir de este momento. De manera que al final del periodo máximo de conservación no se observan diferencias entre los frutos tratados y no tratados.

4. La protección inducida por el CO₂ frente al ataque fúngico durante la conservación y posterior transferencia a temperatura ambiente no parece estar mediada por el incremento en los niveles de mRNA de la STS, que por otro lado fue concomitante con la acumulación de los niveles de *trans*-resveratrol.

5. La incorporación de un estudio cinético a la evaluación de la capacidad antioxidante mediante el método ABTS de cada uno de los antocianos, unido al estudio de la contribución individual de cada antociano a la capacidad antioxidante total del extracto, proporcionan un conocimiento más completo del efecto de las bajas temperaturas y alto CO₂ en el comportamiento de los antocianos.

6. Se ha identificado por primera vez en piel de uva de mesa, la pelargonidina-3-G, que exhibió una alta capacidad antioxidante y cuya acumulación está bajo control de la temperatura y el CO₂. El tratamiento con CO₂ impidió la acumulación de peonidina-3-G, el antociano mayoritario en uva cv. Cardinal y principal responsable del transitorio incremento de antocianos totales y de la capacidad antioxidante total de uvas durante la fase inicial de conservación a 0°C.

7. Este estudio demuestra que la fase inicial de conservación a 0°C de las uvas no tratadas va acompañada de un aumento en los niveles de expresión de los genes que codifican la β -1,3-glucanasa y la quitinasa de clase I. También se observaron aumentos en los niveles de expresión de los transcritos *PAL* y *CHS* como respuesta a las bajas temperaturas, que fueron acompañados de un aumento en el nivel de antocianos y de la capacidad antioxidante.

8. El desajuste metabólico provocado por las bajas temperaturas de conservación se manifestó en un mayor envejecimiento de los tejidos del racimo así como en una mayor y más temprana incidencia de podredumbre. Por el contrario, el tratamiento con CO₂ mantuvo el metabolismo de la baya en condiciones similares a las del fruto recién cosechado permitiendo así el retraso en la aparición de hongos.

9. La efectividad del tratamiento combinado de bajas temperaturas y alta concentración de CO₂ quedaría probada una vez más al prevenir la formación de ROS más que a su inactivación, tal y como se deduce por el patrón de expresión de la APX.

10. Los niveles de expresión de la quitinasa y de la β -1,3-glucanasa fueron menores en los frutos tratados con altos niveles de CO₂, coincidiendo con un menor ataque fúngico lo que permite concluir que el efecto beneficioso del CO₂ en el control de la podredumbre no está mediado por la inducción de PRs.

11. Se ha estudiado la funcionalidad de la quitinasa y de la β -1,3-glucanasa de clase I con el fin de conocer la implicación de estas proteínas en la repuesta de la uva de mesa a las bajas temperaturas y al ataque fúngico. La quitinasa recombinante resultó ser hasta 2,5 veces mas crioprotectora que el BSA y también, fue capaz de inhibir el crecimiento de *B. cinerea* en ensayos *in vitro*. Por otro lado, la β -1,3-glucanasa recombinante presentó una capacidad crioprotectora del orden del BSA. Ambas proteínas no mostraron actividad anticongelante.

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